```
                    GenCore version 5.1.3
                    Copyright (c) 1993 - 2002 Compugen Ltd.

CM protein - protein search, using sw model

Run on:         October 19, 2002, 06:54:51 ; Search time 67 seconds
                                            (without alignments)
                                            1182.562 Million cell updates/sec

Title:          US-09-807-459-2
Perfect score:  2359
Sequence:       1 MAPSDSVGDVTKTLLAASES........DPSKALIRKVSTEADNLLEK 458

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters:    562222

Post-processing: Minimum Match 0%
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      SPTREMBL_19:*
                1:  sp_archea:*
                2:  sp_bacteria:*
                3:  sp_fungi:*
                4:  sp_human:*
                5:  sp_invertebrate:*
                6:  sp_mammal:*
                7:  sp_mhc:*
                8:  sp_organelle:*
                9:  sp_phage:*
                10: sp_plant:*
                11: sp_rodent:*
                12: sp_virus:*
                13: sp_vertebrate:*
                14: sp_unclassified:*
                15: sp_rvirus:*
                16: sp_bacterloverlap:*
                17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2359	100.0	458	5	Q9U5H1	babesia cab
2	2355	99.8	488	5	Q9UA65	babesia cab
3	831.5	35.2	527	5	Q9TVG3	babesia bov
4	830.5	35.2	565	5	Q9U005	babesia bov
5	827.5	35.1	480	5	Q04075	babesia big
6	826.5	35.0	565	5	Q9TVW3	babesia bov
7	826.5	35.0	565	5	O17115	babesia bov
8	826.5	35.0	565	5	Q9U008	babesia bov
9	826.5	35.0	565	5	Q9U007	babesia bov
10	826.5	35.0	565	5	Q9U006	babesia bov
11	825.5	35.0	565	5	Q9U004	babesia bov
12	770.5	32.7	456	5	O17126	babesia can
13	759.5	32.2	496	5	O17256	babesia ovi
14	665.5	28.2	445	5	O17121	babesia bov
15	632.5	26.8	321	5	O17257	babesia ovi
16	574	24.3	273	5	O17255	babesia ovi
17	569.5	24.1	408	5	O17129	babesia div
18	555	23.5	510	5	O15767	babesia big
19	532	22.6	191	5	Q9TVN0	babesia big
20	527	22.3	191	5	O18684	babesia big
21	520	22.0	191	5	O15710	babesia big
22	520	22.0	219	5	O15709	babesia big
23	513	21.7	219	5	O15711	babesia big
24	476	20.2	95	5	Q9UA66	babesia big
25	442.5	18.8	282	5	Q9GUD3	babesia big
26	441.5	18.7	282	5	Q9GUD4	babesia big
27	440.5	18.7	282	5	Q9GUD5	babesia big
28	437.5	18.5	282	5	O15708	babesia big
29	437.5	18.5	301	5	Q9GUD9	babesia big
30	437.5	18.5	304	5	Q9GUD8	babesia big
31	437	18.5	263	5	Q9GN15	babesia big
32	436	18.5	263	5	Q9GUD6	babesia big
33	435.5	18.5	304	5	Q9GNG3	babesia big
34	433.5	18.4	282	5	Q9GUD2	babesia big
35	432.5	18.3	304	5	Q9GUE0	babesia big
36	431.5	18.3	304	5	Q9GUD7	babesia big
37	403.5	17.1	133	5	Q27305	babesia ovi
38	365	15.5	192	5	O17258	babesia ovi
39	346	14.7	69	5	O96431	babesia cab
40	331	14.0	62	5	P90650	babesia cab
41	330.5	14.0	138	5	O27219	babesia cab
42	235.5	10.0	350	5	O15761	babesia ovi
43	234.5	9.9	350	5	O15760	babesia big
44	143.5	6.1	441	12	Q9YV02	melanoplus
45	137.5	5.8	332	2	Q9RGA9	borrelia he

ALIGNMENTS

```
RESULT 1
Q9U5H1
ID   Q9U5H1         PRELIMINARY;      PRT;    458 AA.
AC   Q9U5H1;
DT   01-MAY-2000 (TREMBLrel. 13, Created)
DT   01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE   48KDA MEROZOITE ANTIGEN.
GN   PBC48/31.
OS   Babesia caballi.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX   NCBI_TaxID=5871;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=USDA;
RX   MEDLINE=99454831; PubMed=10523537;
RA   Ikadai H., Xuan X., Igarashi I., Tanaka S., Kameramu T., Nagasawa H.,
RA   Fujisaki K., Suzuki N., Mikami T.;
RT   "Cloning and expression of a 48-kilodalton Babesia caballi merozoite
RT   rhoptry protein and potential use of the recombinant antigen in an
RT   enzyme-linked immunosorbent assay.";
RL   J. Clin. Microbiol. 37:3475-3480(1999).
DR   EMBL; AB017700; BAA83725.1; -.
DR   InterPro; IPR004318; RAP-1.
DR   Pfam; PF03085; RAP-1.
KW   Merozoite.
SQ   SEQUENCE   458 AA;   52138 MW;   A6D33FEEAC66AF2D CRC64;

Query Match             100.0%;  Score 2359;  DB 5;  Length 458;
Best Local Similarity   100.0%;
Matches  458;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPSDSVGDVTKTLLAASESVDSAANAYMINSDMSDYLSAVSDNFAERICSQVPKGSNCS 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPSDSVGDVTKTLLAASESVDSAANAYMINSDMSDYLSAVSDNFAERICSQVPKGSNCS 60

Qy         61 ASVSAYMSRCAKQDCLTLOSLKYPLEAKXQPLTLPDPYQLEAAFILFKESDANPANSTEK 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ASVSAYMSRCAKQDCLTLOSLKYPLEARYQPLTLPDPYQLEAAFILFKESDANPANSTEK 120
```

```
RESULT 2
Q9UA65

ID   Q9UA65       PRELIMINARY;     PRT;   488 AA.
AC   Q9UA65;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   RHOPTRY-ASSOCIATED PROTEIN 1.
GN   RAP-1.
OS   Babesia caballi.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX   NCBI_TaxID=5871;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99294770; PubMed=10364599;
RA   Kappmeyer L.S., Perryman L.E., Hines S.A., Baszler T.V., Katz J.B.,
RA   Hennager S.G., Knowles D.P.;
RT   "Detection of equine antibodies to babesia caballi by recombinant B.
RT   caballi rhoptry-associated protein 1 in a competitive-inhibition
RT   enzyme-linked immunosorbent assay."
RL   Clin. Microbiol. 37.2285-2290(1999).
DR   EMBL; AF092736; AAD40981.1; -.
DR   InterPro; IPR004318; -.
DR   Pfam; PF03085; RAP-1; 1.
SEQUENCE   488 AA;   55194 MW;  88EDA252D16C77E CRC64;

Query Match           99.8%;  Score 2355;  DB 5;  Length 488;
Best Local Similarity 99.8%;
Matches  457;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy    1 MAPSDSVGDVTKILLAASESVDSAANAYMINSDMSDYLSAVSDNFAERICSQVPKGSNCS 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   31 MAPSDSVGDVTKILLAASESVDSAANAYMINSDMSDYLSAVSDNFAERICSQVPKGSNCS 90

Qy   61 ASVSAYMSRCAKQDCLTLQSLKYPLEAAKYQPLTLPDPYQLEAAFILFKESDANPANSTEK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   91 ASVSAYMSRCAKQDCLTLQSLKYPLEAKYQPLTLPDPYQLEAAFILFKESDANPANSTEK 150

Qy  121 RFWMRFRRGKNHSYFHDLVFNLLEKNVTRDADATDIENFASRYLYMATLYYKTYTNVDEF 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  151 RFWMRFRRGKNHSYFHDLVFNLLEKNVTRDADATDIENFASRYLYMATLYYKTYTNVDEF 210

Qy  181 GASFFNKLSFTTGLFGWGIKRALKQIIRSNLPLDIGTEHSVSRLQHITSSYKDYMDTQIP 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  211 GASFFNKLSFTTGLFGWGIKRALKQIIRSNLPLDIGTEHSVSRLQHITSSYKDYMDTQIP 270

Qy  241 ALPKFAKRFSLMVVQRLLATVAGYVDTPWYKKWYMKLKNFMVNRVFIPTKKFFNKEIREP 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  271 ALPKFAKRFSLMVVQRLLATVAGYVDTPWYKKWYMKLKNFMVNRVFIPTKKFFNKEIREP 330

Qy  301 SKALKEKVSTDTKDLFENKIGQGTVDFINKEIRDPSKALIRKVSTGAEDLFENKIGQGTV 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  331 SKALKEKVSTDTKDLFENKIGQGTVDFINKEIRDPSKALIRKVSTGAEDLFENKIGQGTV 390

Qy  361 DFINNEIRDPSKALIRKVSTGAEDLFENKIGQGTVDFINKEIRDPSKALIRKVSTEADNLLEK 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  391 DFINNEIRDPSKALIRKVSTGAEDLFENKIGQGTVDFINKEIRDPSKALIRKVSTEADNLLEK 450

Qy  421 FENKIGQGTVDFINKEIRDPSKALIRKVSTEADNLLEK 458
        ||||||||||||||||||||||||||||||||||||||
Db  451 FENKIGQGTVDFINKEIRDPSKALIRKVSTEADNLLEK 488
```

```
RESULT 3
Q9TVG3

ID   Q9TVG3       PRELIMINARY;     PRT;   565 AA.
AC   Q9TVG3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   RHOPTRY ASSOCIATED PROTEIN-1.
GN   RAP-1.
OS   Babesia bovis.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX   NCBI_TaxID=5865;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   STRAIN=UR, AND CG-P;
RA   Suarez C.E., Palmer G.H., Hotel I., McElwain T.F.;
RT   "Structure, sequence, and transcriptional analysis of the Babesia
RT   bovis rap-1 multigene locus.";
RL   Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF030060; AAB84270.1; -.
DR   EMBL; AF030058; AAB84268.1; -.
DR   InterPro; IPR004318; -.
DR   Pfam; PF03085; RAP-1; 1.
SEQUENCE   565 AA;   64933 MW;  F5D769D4E92CDA3F CRC64;

Query Match           35.28%;  Score 831.5;  DB 5;  Length 565;
Best Local Similarity 35.7%;
Matches  179;  Conservative  80;  Mismatches  193;  Indels  49;  Gaps  6;

Qy    1 MAPSDSVGDVTKILLAASESVDSAANAYMINSDMSDYLSAVSDNFAERICSQVPKGSNCS 60
        ||||| |||:||||:|:|.|.|.:|:|||::|||||.||| ||.:|.|:|.||||||:|
Db   31 LAPAEVVGDLIRSTLETADTLMTLRDHMHNITKDMKHVLSNGREQIVNDVCSNAPEDSNCR 90

Qy   61 ASVSAYMSRCAKQDCLTLQSLKYPLEAKYQPLTLPDPYQLEAAFILFKESDANPANSTEK 120
        .:.:.:.|.::..::.:  .:|.::|..:.::|:..|:.|:..:::..:.:...:.::.:
Db   91 -------------------------------------------------------------

Qy  121 RFWMRFRRGKNHSYFHDLVFNLLEKNVTRDADATDIENFASRYLYMATLYYKTYTNVDEF 180
        |||:|||||::|||.|:|:|.||::||:|:||.|||||||:||||:|||||||.|.:.:|
Db  151 REWLRFRNGANHGDYHYFVTGLLNNNVVHEEGTTDVEYLVNKVLYMATMNYKTYLTVNSM 210

Qy  181 GASFFNKLSFTTGLFGWGIKRALKQIIRSNLPLDIGTEHSVSRLQHITSSYKDYMDTQIP 240
        ||||||:|.|.||||||:||:|:|..: :|:|.:.|.:|:|||::.:.:.:.:...:.:|
Db  211 NAKFFNRFSFTTKIFSRRIKQTLSDIIRWNVPEDF-EERSIERITQLITSVEDYMLTQIP 269

Qy  241 ALPKFAKRFSLMVVQRLLATVAGYVDTPWYKKWYMKLKNFMVNRVFIPTKKF------ 292
        ||||||||||||||||||||||||:||||.|||:|..:|:...::|::.:.:
Db  270 TLSKFARRYADMVKRVLLGSLTSYVEAPVWKRWIKFRDFFSKNVTQPTKFIEDTNEVT 329

Qy  293 ------------------FNKEIREPSKALKEKVSTDTKDLFENKIGQGTVD 326
        :.:.:|:::|.::||.:||:.:::|:|.:.::|::.||.:..:|.|.:|.|
Db  330 KNYLKANVAEPTKKFMQDTHEKTKGYLKENVAEPIKTFFKEAPQVTKHFFDDNIGQPTKE 389

Qy  327 FFNKEIRDPSKALKEVSNDAKDLFENKIGQGTVDFINNEIRDPSKALIRKVSTGAEDLF 386
        ||:.:::|.|::.:.:.::|:.:|::.::|.:|.:.:.::|:.:.:.:::|::||:|:.
Db  390 FFEREAPQATKHFLDENIGQPTKEFF-REAPQATKHFLDENTAQPTKEFFKDVPQVTKKVI 448

Qy  181 GASFFNKLSFTTGLFGWGIKRALKQIIRSNLPLDIGTEHSVSRLQHITSSYKDYMDTQIP 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  211 GASFFNKLSFTTGLFGWGIKRALKQIIRSNLPLDIGTEHSVSRLQHITSSYKDYMDTQIP 270
```

Qy 387 ENKIGQGTVDF----------------INNEIRDPSKALIRKVYTEADLFENKIGQGTVDFINK 435
              | || | | ||||| | | ||| | ||| |:|
Db 449 TENIAQPTKEFLREVPHATMKVLNENIAQPAKEIIHEFGTGAKN-FISAAHEGTKQFLNE 507

Qy 436 EIRDPSKALIR-KVSTEADNL 455
              || | | |:| | |
Db 508 TVGQPTKEFLNGALETTKDAL 528

RESULT 4

ID   Q9U005   PRELIMINARY;   PRT;   565 AA.
AC   Q9U005;
DT   01-MAY-2000 (TREMBLrel. 13, Created)
DT   01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE   RHOPTRY ASSOCIATED PROTEIN-1.
GN   RAP-1.
OS   Babesia bovis.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX   NCBI_TaxID=5865;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   STRAIN=UR;
RA   Suarez C.E., Palmer G.H., Hotzel I., McElwain T.F.;
RT   "Structure, sequence, and transcriptional analysis of the Babesia
RT   bovis rap-1 multigene locus.";
RL   Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF030061; AAB84271.1; -.
DR   InterPro; IPR004318; RAP-1.
DR   Pfam; PF03085; RAP-1; 1.
SQ   SEQUENCE 565 AA; 64964 MW; A4D1DF74F5428A83 CRC64;

Query Match   35.2%;   Score 830.5;   DB 5;   Length 565;
Best Local Similarity   35.7%;   Pred. No. 7.6e-47;
Matches 179;   Conservative 80;   Mismatches 193;   Indels 49;   Gaps 6;

Qy   1 MAPSDSVGDVTKTLLAASESVDSAANAYMINSDMSDYLSAVSDNFAERICSQVPKGSNCS 60
             | | | | | ||| |:| ||||| || | ||| | || | ||| | |
Db   31 LAPAEVVGDLTSTLETADTLMTLRDHMHNITIKDMKHVLSNGREQIVNDVCSNAPEDSNCR 90

Qy   61 ASVSAYMSRCAKQDCLTLQSLKYPLEAKYQPLTLPDPYQLEAAFILFKESDANPANSTEK 120
             | ||| | ||| | ||| || |||| |||| |||||||||||||||||||||
Db   91 EVVNNYADRCEMYCGCFTIDNVKPYLYQEYQPLSLPNPYQLDAAFRLFKESASNPAKNSVK 150

Qy 121 RFWMRFRRGKNHSYFHDLVFNLLEKNVIRDADATDIENFASRYLIYMATLYKTIVNVDEF 180
              | | | ||:|||||||||||||| | || |||||||||||||||||||| | | |
Db 151 REWLRFRNGANHGDYHYFVTGLLNNNVHEEGTDVEVLVNKLVLYMATMNYKTYLTVNSM 210

Qy 181 GASFFNKLSFTTGLFGWGIKRALKQIIRSNLPLDIGTEHSVSRLQHITSSYKDYMDTQIP 240
             | |||| | || || || |||||||||||:||||||||||||||||||||||||||
Db 211 NAKFFNRFSFTTKIFSRRIKQTLSDIIRNNVPEDF-EERSIERITQLISSYEDYMLTQIP 269

Qy 241 ALPKFAKRFSLMVVQRLLATVAGYVDTPWYKKWYMKLKNFMVNRVFIPTKKF------- 292
             | || || |||| || ||||| ||||||||||||||||||||||||||||
Db 270 TLSKFARRYADMVKKVLLGSLTSVEAPWYKRWIEKFRDFSKNVTQPTKKFIEDTNEVT 329

Qy 293 ----------FNKEIREPSKALKEKVSTDTKDLFENKIGQGTVD 326
                       |||| ||||| ||| | |||||:| ||||
Db 330 KNYLKANVAEPTKKFMQDTHEKTKGYLKENVAEPTKTFFKEAPQVTKHFFDDNIGQPTKE 389

Qy 327 FFNKEIRDPSKALKEKVSNDAKDLFENKIGQGTVDFINNEIRDPSKALIRKVSTGAEDLF 386
             |||||||||||||||| |:||||||||||||||||| ||||||||||||||| |||
Db 390 FFREAPQATKHFLDENIGQPTKEFF-REAPQATKHFLDENIAQPTKEFFKDVPQVTKKVI 448

Qy 387 ENKIGQGTVDF----------------INNEIRDPSKALIRKVYTEADLFENKIGQGTVDFINK 435
             || ||| || | ||||||||||||||:| | |||
Db 449 TENIAQPTKEFLREVPHATMKVLNENIAQPAKEIIHEFGTGAKN-FISATHEGTKQFLNE 507

Qy 436 EIRDPSKALIR-KVSTEADNL 455
             |||||||||| ||:| | ||
Db 508 TVGQPTKEFLNGALETTKDAL 528

RESULT 5

ID   Q04075   PRELIMINARY;   PRT;   480 AA.
AC   Q04075;
DT   01-NOV-1996 (TREMBLrel. 01, Created)
DT   01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE   MEROZOITE SURFACE PROTEIN.
GN   P58.
OS   Babesia bigemina.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX   NCBI_TaxID=5866;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92049553; PubMed=1944417;
RA   Mishra V.S., Stephens E.B., Dame J.B., Perryman L.E., McGuire T.C.,
RA   McElwain T.F.;
RT   "Immunogenicity and sequence analysis of recombinant p58: A
RT   neutralization sensitive, antigenically conserved Babesia bigemina
RT   merozoite surface protein.";
RL   Mol. Biochem. Parasitol. 47:207-212(1991).
DR   EMBL; M60878; AAA65583.1; -.
DR   InterPro; IPR004318; RAP-1.
DR   Pfam; PF03085; RAP-1; 1.
SQ   SEQUENCE 480 AA; 53794 MW; 46DCC3F0B518C18 CRC64;

Query Match   35.1%;   Score 827.5;   DB 5;   Length 480;
Best Local Similarity   41.8%;   Pred. No. 9.7e-47;
Matches 181;   Conservative 75;   Mismatches 140;   Indels 37;   Gaps 12;

Qy   4 SDSVGDVTKTLLAASESVDSAANAYMINSDMSDYLSAVSDNFAERICSQVPKGSNCSASV 63
             :| |||||||||| |||:| |||||||||||||||||||||||||||||||||| ||
Db   33 AEVVGDVSKTLLEANEVVNAEMEATQVNKDMQSQLSNVKETIVGEVCEKVAGNSTCGGESV 92

Qy   64 SAYMSRCAKQDCLTLQSLKYPLEAKYQPLTLPDPYQLEAAFILFKESDANPANSTEKRFW 123
             :|||||||||||||||||||||||||| ||:||| ||| ||||| ||||||||||
Db   93 IAYVNRCDEGDCLTLDSM----------KYKPLSLPNPYQLDAAFMLFRESDSNPAKNEVKRFW 123

Qy 124 MRFRRGKNHSYFHDLVFNLLEKNVTRDADATDIENFASRYLIYMATLYKTIVNVDERGAS 183
             ||||| || :||||||||||||||:||||| |||||||||||||||||||||:|| |
Db 147 MRSR--SSHGDYHHFVVSLLKRKNVVRDPESNDVENFASQYFMTTLYKTLYKTYTNVDFTRAAK 204

Qy 184 FFNKLSFTTGLFGWGIKRALKQIIRSNLPLDIGTEHSVSRLQHITSSYKDYMDTQIPALP 243
             | || | | | | ||||||:|| :|||| | |||| | |||:|:| | | | |
Db 205 FFNKLAFTTRLFGCFGIQKALKRLVRSNLPVDLGT-HPEATIREIASGYEXYMMTQVPAMT 263

Qy 244 KFAKRFSLMVVQRLLATVAGYVDTPWYKKWYMKLKNFMVNRVFIPTKKFFNKEIREPSK- 302
             || ||:| || ||||| | | | | | :|||| |||:||||| |||||
Db 264 SFAEFSKMATKTLLVTVSDYVHLPAYXRWYRKFKEFIVN-FFTDPAKLIMKHVSQPVKT 322

Qy 303 ALKEKVSTDTKDLFENKIGQGTVDFFNKEIRDPSKALKEKVSNDAKDLFENKI-----G 356
             |||||||| ||||||||||||||||| |||||||| | | | | |:||||
Db 323 AYTKLVPEEHRQAIRNVVGQSTKHIAN-GVRDLSRMIKE---PSQQIIREKLPHYLSKA 377

Qy 357 QGTVDFINNEIRD--PSKALIRKVSTGAEDLFENKIGQGTVDFINNEIRDPSKALIRKVY 414
             ||||||| ||| | ||||||| | | | | ||||||||||| |||||||||||:|
Db 378 KGAVEHVVKVKSVVPIK---QKGDQPSEAAVEETVPSG--DSAETEFEVPEEQYDAVT 432

Qy 415 T-------EADD 419
                     |:||
Db 433 TQEVNSEKVDADD 445

RESULT 6

ID   Q9TVW3   PRELIMINARY;   PRT;   565 AA.
AC   Q9TVW3;
DT   01-MAY-2000 (TREMBLrel. 13, Created)
DT   01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE   RHOPTRY ASSOCIATED PROTEIN-1.

Left block

RESULT 7
ID   Q17115
AC   Q17115;
GN   RAP-1.
OS   Babesia bovis.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX   NCBI_TaxID=5865;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MEXICO MO7;
RX   MEDLINE=98327208; PubMed=9662706;
RA   Suarez C.E., Palmer G.H., Hotzel I., McElwain T.F.;
RT   "Structure, sequence, and transcriptional analysis of the Babesia
RT   bovis rap-1 multigene locus.";
RL   Mol. Biochem. Parasitol. 93:215-224(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=T2B, AND R1A;
RA   Suarez C.E., Palmer G.H., Hotzel I., McElwain T.F.;
RT   "Structure, sequence, and transcriptional analysis of the Babesia
RT   bovis rap-1 multigene locus.";
RL   Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF027149; AAC27387.1; -.
DR   EMBL; AF030054; AAB84264.1; -.
DR   EMBL; AF030055; AAB84265.1; -.
DR   EMBL; AF030059; AAB84269.1; -.
DR   EMBL; AF027149; AAC27386.1; -.
DR   InterPro; IPR004318; RAP-1.
DR   Pfam; PF03085; RAP-1; 1.
SQ   SEQUENCE   565 AA; 64933 MW; 6AC555E3B6F55615 CRC64;

Query Match   35.0%;   Score 826.5; DB 5; Length 565;
Best Local Similarity   35.5%;   Pred. No. 1.4e-46;
Matches 178; Conservative 79; Mismatches 195; Indels 49; Gaps   6;

```
Qy    1 MAPSDSVGDVTKTLLAASESVDSAAANAYMINSDMSDYLSAVSDNFAERICSQVPKGSNCS 60
          :|||  |::| | :| |||||
Db   31 LAPAEVVGDLTSTLETADTLMTLRDHMHNITKDMKHVLSNGREQIVNDVCSNAPEDSNCR 90

Qy   61 ASVSAYMSRCAKQDCLTLQSLKYPLEAKYQPLTLPDPYQLEAAFILFKESDANPANSTEK 120
         |  : ::| | |: | |: ||||| | ||| ||| |||:|||:  |||||:|||| |::|
Db   91 EVVNNYADRCEMYGCFTIDNVKYPLYQEYQPLSLPNPYQLDAAFLRFKESASNPAKNSVK 150

Qy  121 RFWMRFRRGKNHSYFHDLVFNLLEKNVTRDADATDIENFASRYLYMATLYYKTYTNVDEF 180
         |:|:|| |:|| ||:  | || : |||:|| |  |||||:||||||:  |||| ||:|
Db  151 REWLRFRNGANHGDYHYFVTGLLNNNVHEEGTDVEYLVNKVLYMATMNYKTYLTVNSM 210

Qy  181 GASFENKLSFTTGLFGWGIKRALKQIIRSNLPLDIGTEHSVSRLQHITSSYKDYMDTQIP 240
          | ||| ||| : : | : ||::| |:: :|| | ||::: :: |:|||||:|||:|:||
Db  211 NAKFFNRFSFTTKIFSRRIRQTLSDIIRWNVPEDF-EERSIERITQLTSSYEDYMLTQIP 269

Qy  241 ALPKFAKRFSLMVVQRLLATVAGYVDTPWYKKWYMKLKNFMVNRVFIPTKKF------- 292
          | ||| :|  ||::||| : | ||  |||:|| |:|:|||:|||  |  |
Db  270 TLSKFARRYADMVKKVLLGSLTSYVEAPVWYKRWIKKFRDFFSKNVTQPTKFIEDTNEVT 329

Qy  293 ------------------FNKEIREPSKALKEKVSTDTTKDLFENKIGQGTVD 326
                           |||||| ||||:||||:|   ||||||:||||||
Db  330 KNYLKANVAEPTKKFMQDTHEKTKGYLKENVAEPTKTFFKEAPQVTKHFFDENIGQPTKE 389

Qy  327 FFNKEIRDPSKALKEKVSNDAKDLFENKIGQGTVDFINNEIRDPSKALIRKVYSTGAEDLF 386
         || :: |  |:|::|| :| :| | ||||:|  : |:  ||:|  |||:|:|   | |:|
Db  390 FFREAPQATKHFLDENIGQPTKEFF-REAPQATKHFLGENIAQPTKEEFKDVPQVTKKVI 448

Qy  387 ENKIGQGTVDF-----------INNEIRDPSKALIRKVYTEADDLFENKIGQGTVDFINK 435
         | ||||  :  :          ||||||:| |||:|:|: || || | |||:|  : |:
Db  449 TENIAQPTKEFRREVPHATMKVLNENIAQPAKEIIHEFGTGAKN-FISAAHEGTKQFLNE 507

Qy  436 EIRDPSKALIR-KVSTEADNL 455
         |:  |:|| :| |||  || |
Db  508 TVGQPTKEFLNGALETTKDAL 528
```

PRELIMINARY; PRT; 565 AA.

Middle block

DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MEROZOITE SURFACE PROTEIN.
BV60.
GN   RAP-1.
OS   Babesia bovis.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX   NCBI_TaxID=5865;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MO7; TISSUE=LAMBDA-ZAP II LAMBDA-GT11;
RX   MEDLINE=91304520; PubMed=1712911;
RA   Suarez C.E., Palmer G.H., Jasmer D.P., Hines S.A., Perryman L.E.,
RA   McElwain T.F.;
RT   "Characterization of the gene encoding a 60-kilodalton Babesia bovis
RT   merozoite protein with conserved and surface exposed epitopes.";
RL   Mol. Biochem. Parasitol. 46:45-52(1991).
DR   EMBL; M38218; AAA62695.1; -.
DR   InterPro; IPR004318; RAP-1.
DR   Pfam; PF03085; RAP-1; 1.
SQ   SEQUENCE   565 AA; 64976 MW; B77D347DCF12C874 CRC64;

Query Match   35.0%;   Score 826.5; DB 5; Length 565;
Best Local Similarity   35.5%;   Pred. No. 1.4e-46;
Matches 178; Conservative 79; Mismatches 195; Indels 49; Gaps   6;

```
Qy    1 MAPSDSVGDVTKTLLAASESVDSAAANAYMINSDMSDYLSAVSDNFAERICSQVPKGSNCS 60
          :|||  |::| | :| |||||
Db   31 LAPAEVVGDLTSTLETADTLMTLRDHMHNITKDMKHVLSNGREQIVNDVCSNAPEDSNCR 90

Qy   61 ASVSAYMSRCAKQDCLTLQSLKYPLEAKYQPLTLPDPYQLEAAFILFKESDANPANSTEK 120
         |  : ::| | |: | |: ||||| | ||| ||| |||:|||:  |||||:|||| |::|
Db   91 EVVNNYADRCEMYGCFTIDNVKYPLYQEYQPLSLPNPYQLDAAFLRFKESASNPAKNSVK 150

Qy  121 RFWMRFRRGKNHSYFHDLVFNLLEKNVTRDADATDIENFASRYLYMATLYYKTYTNVDEF 180
         |:|:|| |:|| ||:  | || : |||:|| |  |||||:||||||:  |||| ||:|
Db  151 REWLRFRNGANHGDYHYFVTGLLNNNVHEEGTDVEYLVNKVLYMATMNYKTYLTVNSM 210

Qy  181 GASFENKLSFTTGLFGWGIKRALKQIIRSNLPLDIGTEHSVSRLQHITSSYKDYMDTQIP 240
          | ||| ||| : : | : ||::| |:: :|| | ||::: :: |:|||||:|||:|:||
Db  211 NAKFFNRFSFTTKIFSRRIRQTLSDIIRWNVPEDF-EERSIERITQLTSSYEDYMLTQIP 269

Qy  241 ALPKFAKRFSLMVVQRLLATVAGYVDTPWYKKWYMKLKNFMVNRVFIPTKKF------- 292
          | ||| :|  ||::||| : | ||  |||:|| |:|:|||:|||  |  |
Db  270 TLSKFARRYADMVKKVLLGSLTSYVEAPVWYKRWIKKFRDFFSKNVTQPTKFIEDTNEVT 329

Qy  293 ------------------FNKEIREPSKALKEKVSTDTTKDLFENKIGQGTVD 326
                           |||||| ||||:||||:|   ||||||:||||||
Db  330 KNYLKANVAEPTKKFMQDTHEKTKGYLKENVAEPTKTFFKEAPQVTKHFFDENIGQPTKE 389

Qy  327 FFNKEIRDPSKALKEKVSNDAKDLFENKIGQGTVDFINNEIRDPSKALIRKVYSTGAEDLF 386
         || :: |  |:|::|| :| :| | ||||:|  : |:  ||:|  |||:|:|   | |:|
Db  390 FFREAPQATKHFLDENIGQPTKEFF-REAPQATKHFLGENIAQPTKEEFKDVPQVTKKVI 448

Qy  387 ENKIGQGTVDF-----------INNEIRDPSKALIRKVYTEADDLFENKIGQGTVDFINK 435
         | ||||  :  :          ||||||:| |||:|:|: || || | |||:|  : |:
Db  449 TENIAQPTKEFRREVPHATMKVLNENIAQPAKEIIHEFGTGAKN-FISAAHEGTKQFLNE 507

Qy  436 EIRDPSKALIR-KVSTEADNL 455
         |:  |:|| :| |||  || |
Db  508 TVGQPTKEFLNGALETTKDAL 528
```

Right block

RESULT 8
ID   Q9U008
AC   Q9U008;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   RHOPTRY ASSOCIATED PROTEIN-1.
GN   RAP-1.
OS   Babesia bovis.

PRELIMINARY; PRT; 565 AA.

RESULT 9

```
ID   Q9U007      PRELIMINARY;      PRT;   565 AA.
AC   Q9U007;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   RHOPTRY ASSOCIATED PROTEIN-1.
GN   RAP-1.
OS   Babesia bovis.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX   NCBI_TaxID=5865;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S2P;
RA   Suarez C.E., Palmer G.H., Hotzel I., McElwain T.F.;
RT   "Structure, sequence, and transcriptional analysis of the Babesia
RT   bovis rap-1 multigene locus.";
RL   Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF030053; AAB84263.1; -.
DR   InterPro; IPR004318; RAP-1.
DR   Pfam; PF03085; RAP-1; 1.
SQ   SEQUENCE   565 AA;  64947 MW;  BB57E4A97654488 CRC64;
```

```
Query Match             35.0%;  Score 826.5;  DB 5;  Length 565;
Best Local Similarity   35.5%;  Pred. No. 1.4e-46;
Matches  178;  Conservative  79;  Mismatches  195;  Indels  49;  Gaps  6;
```

```
Qy    1 MAPSDSVGDVTKTLLAASESVDSAANAYMINSDMSDYLSAVSDNFAERICSQVPKGSNCS 60
Db   31 LAPAEVGDLTSTLETADTLMTLRDHMHNITKDMKHVLSNGREQIVNDVCSNAPEDSNCR 90

Qy   61 ASVSAYMSRCAKQDCLTLQSLKYPLEAKYQPLTLPDPYQLEAAFILFKESDANPANSTEK 120
Db   91 EVVNNYADRCEMYGCFTIDNVKPLYQEYQPLSLPNYQLDAAFRLFKESASNPAKNSVK 150

Qy  121 RFWMRFRRGKNHSYFHDLVFNLLEKNVTRDADATDIENFASRYLYMATLYYKTYTNVDEF 180
Db  151 REWLRFRNGANHGDYHYFVTGLLNNNVHEEGTTDVEYLVNKVLYMATMNYKTYLTVNSM 210

Qy  181 GASFFNKLSFTTGLFPGWGIKRALKQIIRSNLPLDIGTEHSVSRLQHITSSYKDYMDTQIP 240
Db  211 NAKFFNFRSFTTKIFSRRIRQTLSDIIRWNVPEDF-EERSIERITOLTSSYEDYMLTQIP 269

Qy  241 ALPKFAKRFSLMVVQRLLATVAGYVDTPWYKKWYMKLKNFMVNRVFIPTKKF------- 292
Db  270 TLSKFARRYADMVKKVLLGSLTSYVEAPWYKRWIKKFRDFFSKNVTQPTKKFIEDTNEVT 329

Qy  293 ---------FNKEIREPSKALKEKVSTDIKDLFENKIGQGTVD 326
Db  330 KNYLKANVAEPTKKFMQDDTHEKTGYLKENVAEPKTFFKEAPQITKHFFDENIGQPTKE 389

Qy  327 FFNKEIRDPSKALKEKVSNDAKDLFENKIGQGTVDFINNEIRDPSKALIRKVSTGAEDLF 386
Db  390 FFREAPQATKHFLDENIGQPTKEFF-REAPQATKHFLGENIAQPTKEFFKDVPQVTKKVI 448

Qy  387 ENKIGQGTVDF----------INNEIRDPSKALIRKVYTEADDLFENKIGQGTVDFINK 435
Db  449 TENIAQPTKEFLREVPHATMKVLNENIAQPAKEIIHEFGTGAKN-FISAAHEGTKQFLNE 507

Qy  436 EIRDPSKALIR-KVSTEADNL 455
Db  508 TVGQPTKEFLNGALETTKDAL 528
```

RESULT 10

```
ID   Q9U006      PRELIMINARY;      PRT;   565 AA.
AC   Q9U006;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   RHOPTRY ASSOCIATED PROTEIN-1.
GN   RAP-1.
OS   Babesia bovis.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX   NCBI_TaxID=5865;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CG-P;
RA   Suarez C.E., Palmer G.H., Hotzel I., McElwain T.F.;
RT   "Structure, sequence, and transcriptional analysis of the Babesia
RT   bovis rap-1 multigene locus.";
RL   Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF030056; AAB84266.1; -.
DR   InterPro; IPR004318; RAP-1.
DR   Pfam; PF03085; RAP-1; 1.
SQ   SEQUENCE   565 AA;  64934 MW;  AC1E38520B438D7A CRC64;
```

```
Query Match             35.0%;  Score 826.5;  DB 5;  Length 565;
Best Local Similarity   35.5%;  Pred. No. 1.4e-46;
Matches  178;  Conservative  79;  Mismatches  195;  Indels  49;  Gaps  6;
```

```
Qy    1 MAPSDSVGDVTKTLLAASESVDSAANAYMINSDMSDYLSAVSDNFAERICSQVPKGSNCS 60
Db   31 LAPAEVGDLTSTLETADTLMTLRDHMHNITKDMKHVLSNGREQIVNDVCSNAPEDSNCR 90

Qy   61 ASVSAYMSRCAKQDCLTLQSLKYPLEAKYQPLTLPDPYQLEAAFILFKESDANPANSTEK 120
Db   91 EVVNNYADRCEMYGCFTIDNVKPLYQEYQPLSLPNYQLDAAFRLFKESASNPAKNSVK 150

Qy  121 RFWMRFRRGKNHSYFHDLVFNLLEKNVTRDADATDIENFASRYLYMATLYYKTYTNVDEF 180
Db  151 REWLRFRNGANHGDYHYFVTGLLNNNVHEEGTTDVEYLVNKVLYMATMNYKTYLTVNSM 210

Qy  181 GASFFNKLSFTTGLFPGWGIKRALKQIIRSNLPLDIGTEHSVSRLQHITSSYKDYMDTQIP 240
Db  211 NAKFFNFRSFTTKIFSRRIRQTLSDIIRWNVPEDF-EERSIERITOLTSSYEDYMLTQIP 269

Qy  241 ALPKFAKRFSLMVVQRLLATVAGYVDTPWYKKWYMKLKNFMVNRVFIPTKKF------- 292
Db  270 TLSKFARRYADMVKKVLLGSLTSYVEAPWYKRWIKKFRDFFSKNVTQPTKKFIEDTNEVT 329

Qy  293 ---------FNKEIREPSKALKEKVSTDIKDLFENKIGQGTVD 326
Db  330 KNYLKANVAEPTKKFMQDDTHEKTGYLKENVAEPKTFFKEAPQITKHFFDENIGQPTKE 389

Qy  327 FFNKEIRDPSKALKEKVSNDAKDLFENKIGQGTVDFINNEIRDPSKALIRKVSTGAEDLF 386
Db  390 FFREAPQATKHFLDENIGQPTKEFF-REAPQATKHFLGENIAQPTKEFFKDVPQVTKKVI 448

Qy  387 ENKIGQGTVDF----------INNEIRDPSKALIRKVYTEADDLFENKIGQGTVDFINK 435
Db  449 TENIAQPTKEFLREVPHATMKVLNENIAQPAKEIIHEFGTGAKN-FISAAHEGTKQFLNE 507

Qy  436 EIRDPSKALIR-KVSTEADNL 455
Db  508 TVGQPTKEFLNGALETTKDAL 528
```

```
ID   ...   (continued)
DR   EMBL; AF030057; AAB84267.1; -.
DR   InterPro; IPR004318; RAP-1.
DR   Pfam; PF03085; RAP-1; 1.
SQ   SEQUENCE   565 AA;  64906 MW;  5A60A059E931D3B9 CRC64;

Query Match             35.0%;  Score 826.5;  DB 5;  Length 565;
Best Local Similarity   35.5%;  Pred. No. 1.4e-46;
```

```
Matches 178;    Conservative 80;    Mismatches 194;    Indels 49;    Gaps 6;

Qy    1 MAPSDSVGDVTKTLLAASESVDSAANAYMINSDMSDYLSAVSDNFAERICSQVPKGSNCS 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   31 LAPAEVVGDLTSTLETADTLMTLRDHMINITKDMKHVLSNGREQIVNDVCSNAPEDSNCR 90

Qy   61 ASVSAYMSRCAKQDCLITLQSLKYPLEAKYQPLTLPDPYQLEAAFILFKESDANPANSTEK 120
        ||: |||||||||||||:||:  ||||||||||||: |:|| |||||||||||||||||||
Db   91 EVVNNYADRCEMYGCFIIDNVKYPLYQEYQPLSLPNPYQLDAAFRLFKESASNPAKNSVK 150

Qy  121 RFWMRFRRGKNHSYFHDLVFNLLEKNVTRDADATDIENFASRYLYMATLIYKTYTNVDEF 180
        | :||||:|||||||||||||:|||:||||||||||||||||||| ||||||||||||||
Db  151 REWLRFRNGANHGDYHYFVTGLLNNNVHEEGTTDVEYLVNKYLYMATMNYKTYLTVNSM 210

Qy  181 GASFFNKLSFTTGLFGWGIKRALKQIIRSNLPLDIGTEHSVSRLQHITSSYKDYMDTQIP 240
        |||||||||||||||||||| | ||||:|||||:|||||||:|||:|||||||:|||||||
Db  211 NAKFFNRFSFTTKIFSRRIKQTLSDIIRWNVPEDF-EERSIERITQOLTSSYEDVMLTQIP 269

Qy  241 ALPKFAKRFSLMVVQRLLATVAGYVDFPWYKKWYMKLKNFMVNRVFIPTKKF------ 292
        ||||||||||||:|||||||||||||: |||  |::||:|||||||||||||
Db  270 TLSKFARRYADMVKKVLLGSLTSYVEAPWYKRWIKKFRDFFSKNVTQPTKKFIEDTNEVT 329

Qy  293 -----FNKEIREPSKA---------------LKEKVSTDKDLFENKIGQGTVD 326
             ||||||||||||||              |||:||||||||||||||||||
Db  330 KNYLKANVAEPTKKFMQDTHEKTKGYLKENVAEPTKTFFKEAPQVTKHFFDDNTGQPTKE 389

Qy  327 FFNKEIRDPSKALIKEKVSNDADLFENKIGQGTVDFINNEIRDPSKALIRKVVTEADDLF 386
        |||||||||||||||||||||||||||||||||||| ||||||||||||||||:||||||
Db  390 FFREAPQATKHFLDENIGQPTKEFF-REAPQATKHFLDENIAQPTKEFFKDVPQVTKKVI 448

Qy  387 ENKIGQGTVDF-------------INNEIRDPSKALIRKVYTEADDLFENKIGQGTVDFINK 435
        |:|||||||||             ||||||||||||||||||:||||||||||||||||||
Db  449 TENIAQPTKEFLREVPHATMKVLNENIAQPAKEIIHEFGTGAKN-FISAAHEGTKQFLNE 507

Qy  436 EIRDPSKALIR-KVSTEADNL 455
        ||||||||||| |:||||||
Db  508 TVGQPTKEFLNGALETTKDAL 528
```

RESULT 11

```
ID   Q9U004        PRELIMINARY;      PRT;   565 AA.
AC   Q9U004;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   RHOPTRY ASSOCIATED PROTEIN-1.
GN   RAP-1.
OS   Babesia bovis.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX   NCBI_TaxID=5865;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=R1A;
RA   Suarez C.E., Palmer G.H., Hotzel I., McElwain T.F.;
RT   "Structure, sequence, and transcriptional analysis of the Babesia
RT   bovis rap-1 multigene locus.";
RL   Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF030062; AAB84272.1; -.
DR   InterPro; IPR004318; RAP-1.
DR   Pfam; PF03085; RAP-1; 1.
SQ   SEQUENCE   565 AA;  64979 MW;  7F5E0019DEBA1892 CRC64;
```

Query Match   35.0%;   Score 825.5;   DB 5;   Length 565;
Best Local Similarity   36.5%;   Pred. No. 1.6e-46;
   Matches 183;   Conservative 77;   Mismatches 192;   Indels 49;   Gaps 8;

```
Qy    1 MAPSDSVGDVTKTLLAASESVDSAANAYMINSDMSDYLSAVSDNFAERICSQVPKGSNCS 60
        ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   31 LAPAEVVGDLTSTLETADTLMTLRDHMINITKDMKHVLSNGREQIVNDVCSNAPEDSNCR 90

Qy   61 ASVSAYMSRCAKQDCLITLQSLKYPLEAKYQPLTLPDPYQLEAAFILFKESDANPANSTEK 120
        ||: |||||||||||||:||:  ||||||||||||: |:|| |||||||||||||||||||
```

RESULT 12

```
ID   Q17126        PRELIMINARY;      PRT;   456 AA.
AC   Q17126;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   RHOPTRY PROTEIN.
OS   Babesia canis.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX   NCBI_TaxID=5867;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=TOWNSVILLE;
RX   MEDLINE=93165069; PubMed=8433711;
RA   Dalrymple B.P., Casu R.E., Peters J.M., Dimmock C., Gale K.R., Bose R.,
RA   Wright I.G.;
RT   "Characterisation of a family of multi-copy genes encoding rhoptry
RT   protein homologues in Babesia bovis, Babesia ovis and Babesia canis.";
RL   Mol. Biochem. Parasitol. 57:181-192(1993).
DR   EMBL; M91168; AAA27807.1; -.
DR   InterPro; IPR001064; Crystallin.
DR   InterPro; IPR004318; RAP-1.
DR   Pfam; PF03085; RAP-1; 1.
DR   PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
SQ   SEQUENCE   456 AA;  52470 MW;  87C5C7CA40A8DB924 CRC64;
```

Query Match   32.7%;   Score 770.5;   DB 5;   Length 456;
Best Local Similarity   35.0%;   Pred. No. 5.1e-43;
   Matches 161;   Conservative 95;   Mismatches 161;   Indels 43;   Gaps 9;

```
Qy    1 MAPSDSVGDVTKTLLAASESVDSAANAYMINSDMSDYLSAVSDNFAERICSQVPKGSNCS 60
        :: |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db   31 LSKSDGAEKTLSTLLNVDASTRAALEGYRMNAAMANFSNGRREEEEAAVCGNIAEETECQ 90

Qy   61 ASVSAYMSRCAKQDCLITLQSLKYPLEAKYQPLTLPDPYQLEAAFILFKESDANPANSTEK 120
        ||:|:|:: |||| || ::|||:||:|:|||||:||:|||||||||| :|::|| ||:: |
Db   91 KSVAEYVESCVRYDCFSIENQKYPQEKEYQPLTLPNPYQLTFVRNSESNPIKNPTE 150

Qy  121 RFWMRFRRGKNHSYFHDLVFNLLEKNVTRDADATDIENFASRYLYMATLIYKTYTNVDEF 180
        ||||||||| ||||| | :|  ||||||||||||||||||||||||||:|:|||  ||||
Db  151 AFWMRFRHGGRYGAYHNFLVNILYKNLSDSMVDDNLEGFVRKYAYMATMYKTYTALDVV 210
```

```
Qy   181  GASFFNKLSFTTGLFGWGIKRALKQIIRSNLPLDIGTEHSVSRLQHITSSYKDYMDTQIP  240
          |||:||  |||  |:|:| ||| :|||||  || |:|| |:||:|| :||||: |:|
Db   211  NARIINKIAFSRHLFGRQIRNALTNIIRSNIPEDG-KINVDLRHVMGGYEYMMKQVP    269

Qy   241  ALPKFAKRFSLMVVQRLLATVAGYDYPWYKKWYMKLKNFMVNRVFIPTKFKFFNKEIREP  300
          :|| ||||  :| |:| |:: ||| ||| :| ||:|||| ||  ||::|| |: :| ||
Db   270  SLPNFAKKYAGMVVKSLIKNVGAYQKQPWFKKLNNQIRNFFVNKIHEPTKEFFVNKIHEP  329

Qy   301  SKALKEKVSTDTKDLFENKIGQGTVDFFNKEIRDPSKALKEKVSNDAKDLFENKIGQGTV  360
          ||||||| | |  :::  |: : |||| :||||||||| :: |||:||:|| |||||||||
Db   330  -------------------TKEFFVNKLHEPTKEFFVNKIHEPT-----------------  367

Qy   361  DFINNEIRDPSKALIRKVSTGAEDLFENKIGQGTVDFINNEIRDPSKALIRKVYTEADDL  420
          :| :|:||||||||:: |||||||||  :|| |:
Db   368  EFFVNKLHEPTKEFFSNMVPGAFQKISEKAGR------------HLRS-SKTVVPE--DEPSSS  416

Qy   421  FENKI---GQGTV-DFINKEIRDP--------SKALIRKVSTE  451
          ||:|      |:|  |: ||              :| |||:|
Db   417  LENEAVEDGQLTMGDVTDFEMATPTYEQGSQESLNEVGNE    456
```

RESULT 13

```
Q17256
ID   Q17256;    PRELIMINARY;      PRT;   496 AA.
AC   Q17256;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   RHOPTRY PROTEIN.
OS   Babesia ovis.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX   NCBI_TaxID=5869;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ANKARA;
RX   MEDLINE=93165069; PubMed=8433711;
RA   Dalrymple B.P., Casu R.E., Peters J.M., Dimmock C., Gale K.R., Bose R.,
RA   Wright I.G.;
RT   "Characterisation of a family of multi-copy genes encoding rhoptry
RT   protein homologues in Babesia bovis, Babesia ovis and Babesia canis.";
RL   Mol. Biochem. Parasitol. 57:181-192(1993).
DR   EMBL; M91169; AAA27805.1; -.
DR   InterPro; IPR004318; RAP-1.
DR   Pfam; PF03085; RAP-1; 1.
SQ   SEQUENCE   496 AA;   56892 MW;   2E4020EBD2AF4999 CRC64;

Query Match     32.2%;  Score 759.5;  DB 5;  Length 496;
Best Local Similarity   34.3%;
Matches  161;  Conservative  93;  Pred. No. 3e-42;  Mismatches 173;  Indels 43;  Gaps 8;

Qy     1  MAPSDSVGDVTKTLLAASESVDSAANAYMINSMDSYLSAVSDNFAERICSQVPKGSNCS   60
Db    31  LAPAEAVGDLTHTLKIADEIINAENEHEINRDMHLRLVEEGSKFIDQICQEVAEDSKCR   90

Qy    61  ASVSAYMSRCAKQDCLTLQSLKYPLEAKYQPLTLPDPYQLEAAFILFKESDANPANSTEK  120
Db    91  EQVESYVKRCEENCLQIDEVAYPLNQEYQPLLLPEPYQLDAAFTLFKNCESNPAKNGLK   150

Qy   121  RFWMRFRRGKNHSYFHDLVFNLLEKNVTRDADATDIENFASRYLYMATLYYKTYTNVDEF  180
Db   151  GPWMRYKEGKEHGDYHHFIISLLGKSLVRKDGVTDLEFLVNKLLYMATTYKTLYLIVKKF  210

Qy   181  GASFFNKLSFTTGLFGWGIKRALKQIIRSNLPLDIGTEHSVSRLQHITSSYKDYMDTQIP  240
Db   211  GAEKFFLGENIAQPTKEFFKDVPQVTKKVITENIAQPTKEFLREVPHATMKVLNENIAQP  270

Qy   241  ALPKFAKRFSLMVVQRLLATVAGYDVDTPWYKKWYMKLKNFMVNR----------VFI   287
Db   271  TLSKFAERISDMVMKVLLSSLAGYVKAPVKRWINRFKSLLTGEAYNPDEDIHLLKPIFV  329

Qy   288  PTKKFFNKEIREPSK-ALKEKVSTDTKDLFENKICGQGTVDFFN------KEIRDPSKAL  339
```

RESULT 14

```
Db   330  DTPRNYIKDALRPLRDAVEENIVNPVSDYLRRKQNISRSQNYNDGHHKIDPSLYEPKRPH  389
Qy   340  KEKVSNDAKDLFENKIGQGTVDFINNEIRDPSKALIRKVSTGAEDLFENKIGQGTVDFIN  399
Db   390  IGIAANHARDYIDDKVNK--------------AKELVSAAKDRATGIYADHVKPALSDITN  436
Qy   400  --NEIRDPSKALIRKVY---TEADDLFENKIGQGTVDFINKEIRDPSKA    443
Db   437  VKRNDLLDAVN--IRNILRGSSQDDNNEQEKTEEEKVEEVKPELKQKEYA   484
```

```
Q17121
ID   Q17121;    PRELIMINARY;      PRT;   445 AA.
AC   Q17121;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   RHOPTRY ASSOCIATED PROTEIN 1 (FRAGMENT).
OS   Babesia bovis.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX   NCBI_TaxID=5865;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MO7;
RA   Suarez C.E., Palmer G.H., Hines S.A., McElwain T.F.;
RT   "The Babesia bovis rhoptry associated protein-1 intergenic region
RT   encodes a functional eukaryotic promoter.";
RL   Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; L77326; AAA96414.1; -.
DR   InterPro; IPR004318; RAP-1.
DR   Pfam; PF03085; RAP-1; 1.
FT   NON_TER       1
FT   NON_TER       1
SQ   SEQUENCE   445 AA;   51355 MW;   3A324715F8DAFB7C CRC64;

Query Match     28.2%;  Score 665.5;  DB 5;  Length 445;
Best Local Similarity   35.5%;
Matches  146;  Conservative  64;  Pred. No. 4.1e-36;  Mismatches 152;  Indels 49;  Gaps 6;

Qy    91  PLITLPDPYQLEAAFILFKESDANPANSTEKRFWMRFRRGKNHSYFHDLVFNLLEKNVTRD  150
Db     1  PLSLPNPYQLDAAFRLFKESASNPAKNSVKREWLRFRNGANHGDYHYFVTGLLNNNVVHE    60

Qy   151  ADATDIENFASRYLYMATLYYKTYTNVDEFGASFFNKLSFTTGLFGWGIKRALKQIIRSN  210
Db    61  EGTTDVEYLVNKVLYMAIMNYKITYLTVNSMNAKFFNRFSFTTHIFSRRIRQTLSDIIRWN  120

Qy   211  LPLDIGTEHSVSRLQHITSSYEDYMLTQIPTLSKFARRYADMVKRVLLGSLTSYVEAPWY  270
Db   121  VPEDF--EERSIERITQLIRSSYEDYMLTQIPTLSKFARRYADMVKRVLLGSLTSYVEAPWY  179

Qy   271  KKWYMKLKNFMVNRVFIPTKKF-----------------FNKE                    296
Db   180  KRWIKKFRDFFSKNVTQPTKKFIEDTNEVTKNYLKANVAEPTKKFMQDTHEKTKGYLKEN  239

Qy   297  IREPSKALKEKVSTDTKDLFENKIGQGTVDFFNKEIRDPSKALKEKVSNDAKDLFENKIG  356
Db   240  VAEPTKTFFKEAPQVTKHFFDENIGQPTKEFFREAPQATKHFLDENIQQPTKEFF-REAP  298

Qy   357  QGTVDFINNEIRDPSKALIRKVSTGAEDLFENKIGQGTVDF------------INNEIRDP  405
Db   299  QATKHFLGENIAQPTKEFFKDVPQVTKKVITENIAQPTKEFLREVPHATMKVLNENIAQP  358

Qy   406  SKALIRKVYTEADDLFENKIGQGTVDFINKEIRDPSKALIR-KVSTEADNL    455
Db   359  AKEIIHEFGTGAKN-FISAAHEGTKQFLNETVGQPTKEFLNGALETTKDAL    408
```

RESULT 15

```
Q17257
ID   Q17257;    PRELIMINARY;      PRT;   321 AA.
AC   Q17257;
```

```
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   PUTATIVE (60.2 OR .3) RHOPTRY PROTEIN (FRAGMENT).
OS   Babesia ovis.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX   NCBI_TaxID=5869;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ANKARA;
RX   MEDLINE=93165069; PubMed=8433711;
RA   Dalrymple B.P., Casu R.E., Peters J.M., Dimmock C., Gale K.R., Bose R.,
RA   Wright I.G.;
RT   "Characterisation of a family of multi-copy genes encoding rhoptry
RT   protein homologues in Babesia bovis, Babesia ovis and Babesia canis.";
RL   Mol. Biochem. Parasitol. 57:181-192(1993).
DR   EMBL; M91173; AAA27811.1; -.
DR   InterPro; IPR004318; RAP-1.
DR   Pfam; PF03085; RAP-1; 1.
FT   NON_TER        1      1
SQ   SEQUENCE   321 AA;  37469 MW;  0BFCBE13B13D11108 CRC64;

Query Match             26.8%;  Score 632.5;  DB 5;  Length 321;
Best Local Similarity   47.2%;
Matches  133;  Conservative   45;  Mismatches   87;  Indels   17;  Gaps  6;

Qy    164 LYMATLYKTYTNVDEFGASFENKLSFTTGLFGWGIKRALKQIIRSNLPLDIGTEHSVSR 223
              |||||   ||||       ||||    |  |||||||||        |||  |||| |
Db      2 LYMATTYYKTYLLIVNNSDAKFENRIAFATKIFGFGIKRALKDIVRSNVPEYMG-EHSIER 60

Qy    224 LQHITSSYKDYMDTQIPALPKFAKRFSLMVVQRLLATVAGYVDTPWYKKWYMKLKNFMVN 283
              ||       ||| |  | |||| ||  |||||||||| |  |||| || |||| || ||
Db     61 ISHLAHGYKDYMLTQVPTLSKFAERYSDMVMKVLLSSLAGYVRAPWYKRWFNKVKDFFVN 120

Qy    284 RVFIPTKFFNKEIREPSKA-LKEKVSTDTKDLFENKIGQGTVDFFNKEIRDPSKALKE- 341
              |     ||  ||  |  ||| |    |||| ||  ||||||||||||  |     ||| |
Db    121 KIGKPTKEHFHK--KHPRTAEFFDKMHERTKDFFENKIGAPTKDFFENKIGAPTK 178

Qy    342 KVSNDAKDLFENKIGQGTVDFINNEIRDPSKALIRKVSTGAEDLFENKIGQGTVDFINNE 401
              |  | |||||||||||||||||||  |    | ||||||| |||||||||||||| ||||
Db    179 KIGAPTKDFFENKIGAPTKDFFENKIGAPTK-------DFFENKIGAPTKDFFENK 227

Qy    402 IRDPSKALI-RKVYTEADDLFENKIGQGTVDFINKEIRDPSK 442
              |         | ||||||||| ||||||||||||||||||||
Db    228 LPERTKDFFENKLPEHTKDFFENKIGQGTVDFINKEIRDPSK 269

RESULT 16
ID   Q17255       PRELIMINARY;    PRT;    273 AA.
AC   Q17255;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   RHOPTRY PROTEIN (FRAGMENT).
OS   Babesia ovis.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX   NCBI_TaxID=5869;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ANKARA;
RX   MEDLINE=93165069; PubMed=8433711;
RA   Dalrymple B.P., Casu R.E., Peters J.M., Dimmock C., Gale K.R., Bose R.,
RA   Wright I.G.;
RT   "Characterisation of a family of multi-copy genes encoding rhoptry
RT   protein homologues in Babesia bovis, Babesia ovis and Babesia canis.";
RL   Mol. Biochem. Parasitol. 57:181-192(1993).
DR   EMBL; M91169; AAA27804.1; -.
DR   InterPro; IPR004318; RAP-1.
DR   Pfam; PF03085; RAP-1; 1.
SQ   SEQUENCE   273 AA;  31179 MW;  BE954830D9EAC399 CRC64;

Query Match             24.3%;  Score 574;  DB 5;  Length 273;
Best Local Similarity   43.3%;  Pred. No. 2.3e-30;
Matches  127;  Conservative   41;  Mismatches   73;  Indels   52;  Gaps  7;

Qy    164 LYMATLYKTYTNVDEFGASFENKLSFTTGLFGWGIKRALKQIIRSNLPLDIGTEHSVSR 223
              |||||   ||||       ||||    |  |||||||||        |||  |||  ||
Db      2 LYMATTYYKTYLLIVNNSDAKFENRIAFATKIFGFGIKRALKDIVRSNVPEYMG-EHSIER 60

Qy    224 LQHITSSYKDYMDTQIPALPKFAKRFSLMVVQRLLATVAGYVDTPWYKKWYMKLKNFMVN 283
              |                  ||| |                         |||    | ||
Db     61 KIGKPTKEHFHK--KHPRTAEFFDKMHERTKDFFENKIGAPTKDFFENKIGAPT---- 172

Qy    284 RVFIPTKFFNKEIREPSKA-LKEKVSTDTKDLFENKIGQGTVDFFNKEIRDPSKALKEK 342
              |         |        | |   |   | ||| ||  |                  |
Db    121 ISHLAHGYKDYMLTQVPTLSKFAERYSDMVNKVLLSSLAGYVRAPWYKRWFNKVKDFFVN 120

Qy    343 VSNDAKDLFENKIGQGTVDFINNEIRDPSKALIRKVSTGAEDLFENKIGQGTVDFINNEI 402
                    |||||||||||||||||            ||||||||||||||||||| |
Db    173 ------KDFFENKIGAPTKDFFENK------------DFFENKIGAPTK 216

Qy    403 RDPSKA-------------------------LIRKVYTEADDLFENKIGQGTV 430
                                            ||| | ||||||||||||||||||
Db    217 GAPIKESFENLGHKRPVNWRYISSPQRMNNDSVADVATETVDM-ENHDGGNTV 268

RESULT 17
ID   Q17129       PRELIMINARY;    PRT;    408 AA.
AC   Q17129;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   RHOPTRY ASSOCIATED PROTEIN PRECURSOR.
OS   Babesia divergens.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX   NCBI_TaxID=32595;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DRUMANESS;
RX   MEDLINE=96379225; PubMed=8784776;
RA   Skuce P.J., Mallon T.R., Taylor S.M.;
RT   "Molecular cloning of the rhoptry associated protein homologue of
RT   Babesia divergens.";
RL   Mol. Biochem. Parasitol. 77:99-102(1996).
DR   EMBL; Z49818; CAA89970.1; -.
DR   InterPro; IPR004318; RAP-1.
DR   Pfam; PF03085; RAP-1; 1.
KW   Signal.
FT   SIGNAL         1     21
FT   CHAIN         22    408       POTENTIAL.
FT                                 RHOPTRY ASSOCIATED PROTEIN.
SQ   SEQUENCE   408 AA;  46133 MW;  E74440D6F5C1D151 CRC64;

Query Match             24.1%;  Score 569.5;  DB 5;  Length 408;
Best Local Similarity   36.8%;  Pred. No. 7.6e-30;
Matches  125;  Conservative   59;  Mismatches  137;  Indels   19;  Gaps  6;

Qy      5 DSVGDVTKT----LLAAASESVDSAANAYMINSDMSDYLSAVSDNFAERICSQVPKGSNCS 60
            |       |             |          |   | |    |         |    |
Db     38 DSVAEAIETVDSVMAAIQESVKTMDN------MIAHLSTRSEGFVDDVCQGVNEESQCQ 90

Qy     61 ASVSAYMSRCAKQDCLTLQSLKYPLEAKYQPLTLDPYQLEAAFILFKESDANPANSTEK 120
            || |      |  | |     || |             | | || | |    |    ||
Db     91 ESVRTVSRCIQRGCLKIDHERYAAEKGNQPLAFNPYQVGAAFQLFQECDSDPTQEPNG 150

Qy    121 RFWMRFRRGKNHSYFHDLVFNLLEKNVTRDADATDIENFASRYLMATLLYKTYINVDEF 180
            | |                      |  | | |||   | || ||   |||  |    |
Db    151 NFGMREKHGGRYGAYQSFIMNVVTSSYTQLSDNTEVEDLVNRYLYMATMVYKTYLILDTT 210

Qy    181 GASFENKLSFTTGLFGWGIKRALKQIIRSNLPLDIGTEHSVSRLQHITSSYKDYMDTQIP 240
            ||||||||||||| |||||||||||   |   |||||||||||| |    |||    | |
Db    211 KVHLINKIDFGHHISGKKSIKHMVEKIIRNHLPRDFGI-YSIERLSHISAGYGDYILKQVP 269

Qy    241 ALPKFAKRFSLMVVQRLLATVAGYVDTPWYKKWYMKLKNFMVNRVFIPTKFFNKEIREP 300
            || |||| | | | |  ||| |||||||||||| ||||     | | |           |
Db    241 ALPKFAKRFSLMVVQRLLATVAGYVDTPWYKKWYMKLKNFMVNRVFIPTKFFNKEIREP 300
```

```
Db   270  YMPAFSTRNRMVVDTLHKIIGKYQKMPWVKKWFNSVADFFKNSIGKPIKNLFSK--RAP  327
               :|:   |:|   ||||        ||          ||
Qy   301  SK----ALKEKVSTDTKDLFENKIGQGTVDFFNKEIRDPS  336
               :||||   ||   :||   ||||
Db   328  SSSTEGAWHKKVSHSVKKMLNEKI-PVVKNFFKDGIRKSS  366
```

RESULT 18

```
ID   O15767                PRELIMINARY;      PRT;    510 AA.
AC   O15767;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   RAP-1C.
GN   RAP-1C.
OS   Babesia bigemina.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX   NCBI_TaxID=5866;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MEXICO JG-29;
RA   Hotzel I., Suarez C.E., McElwain T.F., Palmer G.H.;
RT   "Genomic cloning of Babesia bigemina rap-1c gene.";
RL   Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF026272; AAB82596.1; -.
DR   InterPro; IPR004318; RAP-1.
DR   Pfam; PF03085; RAP-1; 1.
SQ   SEQUENCE   510 AA;  57468 MW;  BAE9DCF30C7EB06 CRC64;
```

```
Query Match             23.5%;  Score 555;  DB 5;  Length 510;
Best Local Similarity   28.7%;  Pred. No. 9.2e-29;
Matches   147;  Conservative    80;  Mismatches  177;  Indels  108;  Gaps   15;

Qy     1  MAPS----------DSVGDVTKTLLAASESVDSAANAYMINSDMSDYLSAVSDNFAERICSQV   53
             ||||          :|:  ::|:
Db    31  MAPDHTVEPAVDPVDDDTKOLLEDSEQIEKA----------MOEEIGLINDSIAEMCLGS   81
Qy    54  PKGSNCSASVSAYMSRCAKODCLTLQSLKYPLEARKYQPLTLPDPYQLEAAFILFKESDAN  113
             :|:  ::|  |  |:||  ||| ||| ||||||:  |::||   |||||:  :||||  |
Db    82  KDEHHCASQIAAYVARCKEGNCLTIDAVGKPQNKAYKQLVLPDPYQLHAAPLLFKNCRRN  141
Qy   114  PANSTEKRFWMRFRGRGKNHSYFHDLVFNLLEKNVTRDADATDIENFASRYLIYMATLYKT  173
             |   |  :||  |||:||      |  ||:  ||::|   |:   ||:|:||:  ||||||
Db   142  ESRHWMDRFWMRFKRGRYAAYSFSLNLLRRNLFLGDDKNALHGFVQKYFYMTAIYYKT  201
Qy   174  YTNVDEFGASFFNKLSFTTGLFGWGIKRALKOIIRSNLPLDIGTEHSVSRLQHITSSYKD  233
             |  |  ::| |||||:  ||:||||||||:: ||:  |  |  | :|::|| : |  ||
Db   202  YLSLDAINAKIFNKIALAKHILGPKIKRALRKIVEANKPSAL-QANDVKAIRPLAYGYRQ  260
Qy   234  YMDTQIPALPKFAXRFSLMVVQRLLATVAGYAVDFTPWYKKWYMKLKNFMVNRVFIPTKKFF  293
             || :|||:|  ||:||| ||||:||||  | |||||||:  |||: ||:|||| |||  ::
Db   261  YMASQIPSLPFFAYRFSSMVVTALVDNLTGVKQOPWYKRWFGKVKNLFTGKQ--PSEKAY  318
Qy   294  NKEIREPSKALKEKVSTDTKDLFENKIGQGTVDFFNKEIRDPSKALKEKVSN----  345
             ::   |   :||   ||:          |||||:||| |||||   ||:|
Db   319  -EIDEPIATEEE----TEPVEENK-----SVPGK------VKEKLGNIRENTGIF  357
Qy   346  ---DAK-------------DLFENKIGQGTVDFINNEIRDPSKALIR  376
                |:|             |||||:||||||||||||||||||||  |
Db   358  RKGEAKTRHSHLSEEDIMGSLSSADALLEPVLDVME-KEGEAQ---NEEAGEPEVAAAP  412
Qy   377  KVS--------TGAEDLFENKIGQ--------GTVDFINNEIRD------PSKALI  410
                        ::|||||||||||        |||||:||||||      |||||:
Db   413  KAPESENGELADQVDGASTVASTEMGEEESLEAPKGTQDLMHEDEEQEPESDELPAKRKR  472
Qy   411  RKVYTEADDLFENKIGQGGTVDFINKEIRDPSK  442
             :||| ||||||||||||| ||||||:|||||||
Db   473  KASSTGYKKFFKNILDTGAIKDAASRIGPFKK  504
```

RESULT 19

```
ID   Q9TVN0                PRELIMINARY;      PRT;    191 AA.
AC   Q9TVN0;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   RAP-1 BETA (FRAGMENT).
GN   RAP-1.
OS   Babesia bigemina.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX   NCBI_TaxID=5866;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98135662; PubMed=9476795;
RA   Hotzel I., Suarez C.E., McElwain T.F., Palmer G.H.;
RT   "Genetic variation in the dimorphic regions of rap-1 genes and rap-1
RT   loci of Babesia bigemina.";
RL   Mol. Biochem. Parasitol. 90:479-483(1997).
DR   EMBL; AF014768; AAC47870.2; -.
DR   EMBL; AF014767; AAC47869.2; -.
DR   EMBL; AF014759; AAC47859.2; -.
DR   EMBL; AF014758; AAC47860.2; -.
DR   EMBL; AF014760; AAC47862.2; -.
DR   EMBL; AF014762; AAC47864.2; -.
DR   InterPro; IPR004318; RAP-1.
DR   Pfam; PF03085; RAP-1; 1.
FT   NON_TER       1      1
FT   NON_TER     191    191
SQ   SEQUENCE   191 AA;  21574 MW;  B66D7416F59CA263 CRC64;
```

```
Query Match             22.6%;  Score 532;  DB 5;  Length 191;
Best Local Similarity   52.8%;  Pred. No. 8.4e-28;
Matches   103;  Conservative    32;  Mismatches   52;  Indels   8;  Gaps   2;

Qy     4  SDSVGDVTKTLLAASESVDSAANAYMINSDMSDYLSAVSDNFAERICSQV   63
             :|||||:|||| :|:  |      ||:|    :| ||:::||||||||:
Db     5  AEVVGDVSKTLLEEANEVVNAEMEATQVNKDMQSQLSNVKETIVGEVCEKVAGNSTCGESV   64
Qy    64  SAYMSRCAKODCLTLQSLKYPLEARKYQPLTLPDPYQLEAAFILFKESDANPANSTEKRFW  123
             :|:  |||: |||| ::      |||||| :|||||:||||::||:|||:|||  ::|| |
Db    65  IAYVNRCDEGDCLTLDSM------KYPLSLENPYQLDAAFMLFRESDSNPAKNEVKRRFW  118
Qy   124  MRFRGRGKNHSYFHDLVFNLLEKNVTRDADATDIENFASRYLIYMATLYKTYTNVDEFGAS  183
             ||:|   |:  | :: |  |||:||:||  ||:|||||:||: |:||||||  |:|:|
Db   119  MRSR--SSHGDYHHFVSSLLKKNVVRDPESNDVENFASQYFYWTTLYYKTLYKTLYTVDFTRAAK  176

Qy   184  FFNKLSFTTGLFGWG  198
             |||||:|||:|||:|
Db   177  FFNKLAFTTRLFGFG  191
```

RESULT 20

```
ID   O18684                PRELIMINARY;      PRT;    191 AA.
AC   O18684;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   RAP-1 BETA. (FRAGMENT).
GN   RAP-1.
OS   Babesia bigemina.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX   NCBI_TaxID=5866;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hotzel I., Suarez C.E., McElwain T.F., Palmer G.H.;
RL   Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF014767; AAC47869.2; -.
DR   EMBL; AF014761; AAC47863.2; -.
DR   InterPro; IPR004318; RAP-1.
DR   Pfam; PF03085; RAP-1; 1.
FT   NON_TER       1      1
FT   NON_TER     191    191
SQ   SEQUENCE   191 AA;  21622 MW;  E6666F1DE59CB26F CRC64;
```

```
Qy    8 GDVTKTLLAASESVSDAANAYMINSDMSDYLSAVSDNFAERICSQVPKGSNCSASVSAYM 67
        :|:||| |:|||| |:
Db    9 GDVSKTLLEANEVVNAEMEATQVNKDMQSQLSNVKETIVGEVCEKVAGNSTCGESVIAVV 68

Qy   68 RGKNHSYFHDLVFNLLEKNVTRDADATDIENFASRYLYMATLYYKTYTNVDEFGASFFNK 127
        : :|: |||| |:||||| |||: |:|||||||:||| | ||||||:|||||||||| ||||
Db   69 NRCDEGDCLTLDSM------KYKPLSLPNPYQLDAAFMLFRESDSNPAKNEVKRFWMRSR 122

Qy  128 -SSHGDYHHFVVSLLKKNVVRDPESNDVENFASQYFYMTTLYYKTYLTVDFTAAKFENK 187
        ||||||||||||||||||||||||:|||||||||||||:|
Db  123 --SSHGDYHHFVVSLLKKNVVRDPESNDVENFASQYFYMTTLYYKTYLTVDFTAAKFENK 180

Qy  188 LSFTTGLFGWG 198
        ||:|| |||:|
Db  181 LAFTTRLFGFG 191
```

RESULT 21

```
ID     015710                         PRELIMINARY;      PRT;     191 AA.
AC     015710;
DT     01-JAN-1998 (TrEMBLrel. 05, Created)
DT     01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT     01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE     RAP-1 BETA (FRAGMENT).
OS     Babesia bigemina.
OC     Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX     NCBI_TaxID=5866;
RN     [1]
RP     SEQUENCE FROM N.A.
RX     MEDLINE=98135662; PubMed=9476795;
RA     Hotzel I., Suarez C.E., McElwain T.F., Palmer G.H.;
RT     "Genetic variation in the dimorphic regions of RAP-1 genes and rap-1
RT     loci of Babesia bigemina.";
RL     Mol. Biochem. Parasitol. 90:479-489(1997).
DR     EMBL; AF014764; AAC47866.2; -.
DR     InterPro; IPR004318; RAP-1.
DR     Pfam; PF03085; RAP-1; 1.
FT     NON_TER     1        1
FT     NON_TER   191      191
SQ     SEQUENCE   191 AA;  21786 MW;  66F833D0730DD723 CRC64;
```

Query Match   22.3%;   Score 527; DB 5; Length 191;
Best Local Similarity   53.4%;   Pred. No. 1.8e-27;
Matches 102; Conservative 30; Mismatches 51; Indels 8; Gaps 2;

```
Qy    7 VGDVTKTLLAASESVSDAANAYMINSDMSDYLSAVSDNFAERICSQVPKGSNCSASVSAY 66
        :|| |||||| ||| |: : |: |||||||||||||||||||||||||||||||||||
Db    8 VGDVSKTLLAANEVVNAEMEAAQINEDMKIQLANVKETIVDEVCRKDAGSPTCRKSVIAY 67

Qy   67 MSRCAKQDCLTLQSLKYPLEAKYQPLTLPDPYQLEAAFILFKESDANPANSTEKRFWMRF 126
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   68 VDRCDEGDCLTLDSM------KYKPLSLPNPYQLDAAFMLFRESDSNPAKNEVKRFWMRS 121

Qy  127 RRGKNHSYFHDLVFNLLEKNVTRDADATDIENFASRYLYMATLYYKTYTNVDEFGASFFN 186
        : || ||||||||||||||||||||||||||||||||||||||||:||
Db  122 R--SSHGDYHHFVVSLLKKNVVRDPESNDVENFASQYFYMTTLYYKTYLTVDFTAAKFEN 179

Qy  187 KLSFTTGLFGWG 198
        |||:|| |||:|
Db  180 KLAFTTRLFGFG 191
```

RESULT 22

```
ID     015709                         PRELIMINARY;      PRT;     219 AA.
AC     015709;
DT     01-JAN-1998 (TrEMBLrel. 05, Created)
DT     01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT     01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE     RAP-1 ALPHA (FRAGMENT).
OS     Babesia bigemina.
OC     Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX     NCBI_TaxID=5866;
RN     [1]
RP     SEQUENCE FROM N.A.
RX     MEDLINE=98135662; PubMed=9476795;
RA     Hotzel I., Suarez C.E., McElwain T.F., Palmer G.H.;
RT     "Genetic variation in the dimorphic regions of RAP-1 genes and rap-1
RT     loci of Babesia bigemina.";
RL     Mol. Biochem. Parasitol. 90:479-489(1997).
DR     EMBL; AF014759; AAC47861.2; -.
DR     InterPro; IPR004318; RAP-1.
DR     Pfam; PF03085; RAP-1; 1.
FT     NON_TER     1        1
FT     NON_TER   219      219
SQ     SEQUENCE   219 AA;  24674 MW;  F7720FAE72F7F769 CRC64;
```

Query Match   22.0%;   Score 520; DB 5; Length 219;
Best Local Similarity   51.8%;   Pred. No. 6.2e-27;
Matches 101; Conservative 33; Mismatches 53; Indels 8; Gaps 2;

```
Qy    4 SDSVGDVTKTLLAASESVSDAANAYMINSDMSDYLSAVSDNFAERICSQVPKGSNCSASV 63
        :: ||||||||||| ||| |: : |: |||||||||||||||||||||||||||||||||
Db   33 AEVVGDVSKTLLEANEVVNAEMEATQVNKDMQSQLSNVKETIVDEVCRKDAGNSTCGESV 92

Qy   64 SAYMSRCAKQDCLTLQSLKYPLEAKYQPLTLPDPYQLEAAFILFKESDANPANSTEKRFW 123
        |:|: ||||||||||:|||||||||||| || |||||||:|||||||:||||| | |||
Db   93 IAYVNRCDEGDCLTLDSM------KYKPLSLPNPYQLDAAFMLFRESDSNPAKNEVKRFW 146

Qy  124 MRFRGKNHSYFHDLVFNLLEKNVTRDADATDIENFASRYLYMATLYYKTYTNVDEFGAS 183
        ||| :| : |||| |:|||||||||||||||||||||||||||||||||||||:||
Db  147 MRSR--SSHGDYHHFVVSLLKKNVVRDPESNDVENFASQYFYMTTLYYKTYLTVDFTAAK 204

Qy  184 FFNKLSFTTGLFGWG 198
        ||||||:|| |||:|
Db  205 FFNKLAFTTRLFGFG 219
```

RESULT 23

```
ID     015711                         PRELIMINARY;      PRT;     219 AA.
AC     015711;
DT     01-JAN-1998 (TrEMBLrel. 05, Created)
DT     01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT     01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE     RAP-1 (RAP-1 ALPHA) (FRAGMENT).
OS     Babesia bigemina.
OC     Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX     NCBI_TaxID=5866;
RN     [1]
RP     SEQUENCE FROM N.A.
RX     MEDLINE=98135662; PubMed=9476795;
RA     Hotzel I., Suarez C.E., McElwain T.F., Palmer G.H.;
RT     "Genetic variation in the dimorphic regions of RAP-1 genes and rap-1
RT     loci of Babesia bigemina.";
RL     Mol. Biochem. Parasitol. 90:479-483(1997).
DR     EMBL; AF014765; AAC47867.2; -.
DR     EMBL; AF014763; AAC47865.2; -.
DR     EMBL; AF014766; AAC47868.2; -.
DR     InterPro; IPR004318; RAP-1.
DR     Pfam; PF03085; RAP-1; 1.
FT     NON_TER     1        1
FT     NON_TER   219      219
SQ     SEQUENCE   219 AA;  24693 MW;  DB528E31B7E9127A CRC64;
```

Query Match   21.7%;   Score 513; DB 5; Length 219;
Best Local Similarity   51.8%;   Pred. No. 1.8e-26;

Matches 101; Conservative 32; Mismatches 54; Indels 8; Gaps 2;

```
Qy    4 SDSVGDVTKTLLAASESVDSAANAYMINSDMSDYLSAVSDNFAERICSQVPKGSNCSASV 63
          ||||:|||:||| || | | |||||| | |:| |||
Db   33 AEVVGDVSKTLLAANEVVNAEMEAAQ1NEDMKIQLANVKETIVDEVCRKDAGSPTCRKSV 92

Qy   64 SAYMSRCAKQDCLTLQSSLKYPLEAKYOPLTLPDPYQLEAAFILFKESDANPANSTEKRFW 123
          || | |:| :|| ||
Db   93 IAYVDRCDEGDCLTLDSM------KYKPLSLPNPYQLDAAFMLFRESDSNPAKNEVKCFW 146

Qy  124 MRFRRGKNHSFFHDLVFNLLEKNVTRDADATDIENFASRYLIYMATLYYKTYTNVDEFGAS 183
          : |:| :||||| | ||:||| ||: |:|: | ||||||||||:|
Db  147 MRSR---SSHGDYHHFVVSLLKKNVVRDPESNDVENFASQYFYMTLYYKTYLTVDFTAAK 204

Qy  184 FFNKLSFTTGLFGWG 198
          |||||:|||:|||:|
Db  205 FFNKLAFTTRLFGFG 219
```

RESULT 24
Q9UA66
```
ID   Q9UA66          PRELIMINARY;      PRT;      95 AA.
AC   Q9UA66;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   RHOPTRY-ASSOCIATED PROTEIN 1 (FRAGMENT).
GN   RAP-1.
OS   Babesia caballi.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX   NCBI_TaxID=5871;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=USDA;
RX   MEDLINE=99294770; PubMed=10364599;
RA   Kappmeyer L.S., Perryman L.E., Hines S.A., Baszler T.V., Katz J.B.,
RA   Hennager S.G., Knowles D.P.;
RT   "Detection of equine antibodies to babesia caballi by recombinant B.
RT   caballi rhoptry-associated protein 1 in a competitive-inhibition
RT   enzyme-linked immunosorbent assay.";
RL   J. Clin. Microbiol. 37:2285-2290(1999).
DR   EMBL; AF092735; AAD40080.1; -.
FT   NON_TER       1     1
SQ   SEQUENCE   95 AA;  10719 MW;  771495ADBDEB9FB CRC64;
```

Query Match 20.2%; Score 476; DB 5; Length 95;
Best Local Similarity 100.0%; Pred. No. 1.7e-24;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy  364 NNEIRDPSKALIRKVSTGAEDLFENKIGOGTVDFINNEIRDPSKALIRKVYTEADDLFEN 423
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 NNEIRDPSKALIRKVSTGAEDLFENKIGQGTVDFINNEIRDPSKALIRKVYTEADDLFEN 60

Qy  424 KIGQGTVDFINKEIRDPSKALIRKVSTEADNLLEK 458
          |||||||||||||||||||||||||||||||||||
Db   61 KIGQGTVDFINKEIRDPSKALIRKVSTEADNLLEK 95
```

RESULT 25
Q9GUD3
```
ID   Q9GUD3          PRELIMINARY;      PRT;      282 AA.
AC   Q9GUD3;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   RAP-1 BETA-3.
GN   RAP-1 BETA-3.
OS   Babesia bigemina.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX   NCBI_TaxID=5866;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=UYA;
RX   MEDLINE=98135662; PubMed=9476795;
RA   Hotzel I., Suarez C.E., McElwain T.F., Palmer G.H.;
RT   "Genetic variation in the dimorphic regions of RAP-1 genes and rap-1
RT   loci of Babesia bigemina.";
RL   Mol. Biochem. Parasitol. 90:479-489(1997).
DR   EMBL; AF017297; AAG14915.1; -.
FT   NON_TER       1     1
SQ   SEQUENCE   282 AA;  32568 MW;  F537FA7947DE9BEE CRC64;
```

Query Match 18.8%; Score 442.5; DB 5; Length 282;
Best Local Similarity 35.5%; Pred. No. 1.1e-21;
Matches 105; Conservative 58; Mismatches 102; Indels 31; Gaps 11;

```
Qy  159 FASRYLIYMATLYYKTYTNVDEFGASFFNKLSFTTGLFGWGIKRALKQIIRSNLPLDIGTE 218
          |||||:|| || ||||| |||:| ||||||:|||| :||:| |||||| |:|:|| ||:|
Db    1 FASQYFYMTLYYKTYLTVDFTAAKFFNKLAFTTRLFGFGWGIKRALKQIIRSNLPLDIGT- 59

Qy  219 HSVSRLQHTTSSYKDYMDTQIPALFKPAKRRFSLMVVQRLLATVAGYVDTPWYKKWYMKLK 278
Db   60 HPEATIREIASGYGEYMMTQVPAMTSFAERRSKMATKTLLVTVSDVVHLPAYKRWYRKFK 119

Qy  279 NFMVNRVFIPTKKFFNKEIREPSK-ALKEKVSTDIKDLFENKIGQGTVDFFNKEIRDPSK 337
Db  120 EFIVN-FFTDPAKLIMKHVSQPVKTAYTKLVPEEHRQAIRDVVGQSTKHIAN-GVRDLAR 177
```

RESULT 26
Q9GUD4
```
ID   Q9GUD4          PRELIMINARY;      PRT;      282 AA.
AC   Q9GUD4;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   RAP1 BETA-3 (FRAGMENT).
GN   RAP1 BETA-3.
OS   Babesia bigemina.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX   NCBI_TaxID=5866;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S2P;
RX   MEDLINE=98135662; PubMed=9476795;
RA   Hotzel I., Suarez C.E., McElwain T.F., Palmer G.H.;
RT   "Genetic variation in the dimorphic regions of RAP-1 genes and rap-1
RT   loci of Babesia bigemina.";
RL   Mol. Biochem. Parasitol. 90:479-489(1997).
DR   EMBL; AF017296; AAG14914.1; -.
FT   NON_TER       1     1
SQ   SEQUENCE   282 AA;  32549 MW;  7F9B1A7DA93B6BF1 CRC64;
```

Query Match 18.7%; Score 441.5; DB 5; Length 282;
Best Local Similarity 35.6%; Pred. No. 1.3e-21;
Matches 104; Conservative 60; Mismatches 105; Indels 23; Gaps 9;

```
Qy  159 FASRYLIMATLYYKTYTNVDEFGASFFNKLSFTTGLFGWGIKRALKQIIRSNLPLDIGTE 218
          |||||:|| || ||||| |||:| ||||||:|||| :||:| |||||| |:|:|| ||:|
Db    1 FASQYFYMTLYYKTYLTVDFTAAKFFNKLAFTTRLFGFGWGIKRALKQIIRSNLPLDIGT- 59

Qy  219 HSVSRLQHTTSSYKDYMDTQIPALPKFKAKRRFSLMVVQRLLATVAGYVDTPWYKKWYMKLK 278
Db   60 HPEATIREIASGYGEYMMTQVPAMTSFAERRSKMATKTLLVTVSDVVHLPAYKRWYRKFK 119

Qy  279 NFMVNRVFIPTKKFFNKEIREPSK-ALKEKVSTDIKDLFENKIGQGTVDFFNKEIRDPSK 337
Db  120 EFIVN-FFTDPAKLIMKHVSQPVKTAYTKLVPEEHRQAIRDVVGQSTKHIAN-GVRDLAR 177

Qy  338 ALKEKVSNDAKDLFENKI-----GQGTVDFINNEIRDPSKALIRKVSTGAEDLFENKIG 391
Db  178 MIKE----PSQOIREKLPHYLSKAKGAVEHVVDKVK--SKTFKKRAGESSEESYSD-- 228

Qy  392 QGTVDFINNEIRDPSKALIRKV----YTEAD----DLFENKIGQGTVDFINKEIRD 439
Db  229 -SEEEILKESQYNPAKSVAESAADKDDYLYADWKDAALYKK---YNNWDGVGYEIKD 280
```

```
Qy   338 ALKEKVSNDAKDLFENKI-----GQGTVDFINNEIRDPSKALIRKVSTGAEDLFENKIG 391
         |:||  ||| |:|:||  ||||||||||:||  ||||||||
Db   178 MIKE-----PSQQIIREKLPHYLSKAKGAVEHVVDKVK--SKTLKKRAGESSEESYSDSEE 231

Qy   392 QGTVDFINNEIRDPSKALIRKVVTEAD-----DLFENKIGQGTVDFINKEIRD 439
         ||||||||:||              ||  ||||
Db   232 EILKESQYNPAKSVAESADKDEYLYADWKDAALYKK---YNWVDGVGYEIKD 280
```

RESULT 27
```
ID   Q9GUD5      PRELIMINARY;      PRT;   282 AA.
AC   Q9GUD5;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   RAP1 BETA-3 (FRAGMENT).
GN   RAP-1 BETA-3.
OS   Babesia bigemina.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX   NCBI_TaxID=5866;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CGA;
RX   MEDLINE=98135662; PubMed=9476795;
RA   Hotzel I., Suarez C.E., McElwain T.F., Palmer G.H.;
RT   "Genetic variation in the dimorphic regions of RAP-1 genes and rap-1
RT   loci of Babesia bigemina.";
RL   Mol. Biochem. Parasitol. 90:479-489(1997).
DR   EMBL; AF017295; AAG14913.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   282 AA;   32549 MW;   14EB1A7CED7F7AA4 CRC64;
```

```
Query Match             18.7%;     Score 440.5;   DB 5;    Length 282;
Best Local Similarity   35.5%;     Pred. No. 1.5e-21;
Matches 105; Conservative 58; Mismatches 102; Indels 31; Gaps 11;
```

```
Qy   159 FASRYLYMATLYYKTYTNVDEFGASFFNKLSFTTGLFGWGIKRALKQIIRSNLPLDIGTE 218
         |:|||:|||||||||||||||||||:||||::|:|||||||:|||:||||||||:|:||
Db     1 FASQYFYMTTLYYKTYLTVDFTAAKFFNKLAFTTRLFGFGIQKALKRLVRSNLPVDLGT- 59

Qy   219 HSVSRLQHITSSYKDYMDTQIPALPKFPAKRFSLMVVQRLLATVAGYVDTPWYKKWYMKLK 278
         |:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    60 HPEATIREIASGYGEYMMTQVPAMTSFAERFSKMATKTLLVTVSDYVHLPAYKRWYRKFK 119

Qy   279 NFMVNRVFIPTKKFFNKEIREPSK-ALKEKVSTDTKDLFENKIGQGTVDFFNKEIRDPSK 337
         ||    |||  :||:|:||||  |||||||    |:||||||||||||| ||||
Db   120 EFIVN-FFTDPAKLIMKHVSQPVKTAYTKLVPEEHRQAIRDVVGQSTKHIAN-GVRDLAR 177

Qy   338 ALKEKVSNDAKDLFENKI-----GQGTVDFINNEIRDPSKALIRKVSTGAEDLFENKIG 391
         |:||  ||| |:|:||  ||||||||||:||  ||||||||
Db   178 MIKE-----PSQQIIREKLPHYLSKAKGAVEHVVDKVK--SKTLKKRAGESSEESYSD--- 228

Qy   392 QGTVDFINNEIRDPSKALIRKV-----YTEAD-----DLFENKIGQGTVDFINKEIRD 439
         ||||||||:||              ||  ||||
Db   229 -SEEEILKESQYNPAKSVAESADKDDYLYADWKDAALYKK---YNWVDGVGYEIKD 280
```

RESULT 28
```
ID   O15708      PRELIMINARY;      PRT;   282 AA.
AC   O15708;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   RHOPTRY ASSOCIATED PROTEIN-1 (FRAGMENT).
GN   RAP-1.
OS   Babesia bigemina.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX   NCBI_TaxID=5866;
RN   [1]
RP   SEQUENCE FROM N.A.
```

```
RX   MEDLINE=98135662; PubMed=9476795;
RA   Hotzel I., Suarez C.E., McElwain T.F., Palmer G.H.;
RT   "Genetic variation in the dimorphic regions of RAP-1 genes and rap-1
RT   loci of Babesia bigemina.";
RL   Mol. Biochem. Parasitol. 90:479-489(1997).
DR   EMBL; AF014406; AAC47858.1; -.
DR   InterPro; IPR004318; RAP-1.
FT   Pfam; PF03085; RAP-1; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   282 AA;   32569 MW;   F5391A7DA7D49BEE CRC64;
```

```
Query Match             18.5%;     Score 437.5;   DB 5;    Length 282;
Best Local Similarity   35.1%;     Pred. No. 2.3e-21;
Matches 104; Conservative 59; Mismatches 102; Indels 31; Gaps 11;
```

```
Qy   159 FASRYLYMATLYYKTYTNVDEFGASFFNKLSFTTGLFGWGIKRALKQIIRSNLPLDIGTE 218
         |:|||:|||||||||||||||||||:||||::|:|||||||:|||:||||||||:|:||
Db     1 FASQYFYMTTLYYKTYLTVDFTAAKFFNKLAFTTRLFGFGIQKALKRLVRSNLPVDLGT- 59

Qy   219 HSVSRLQHITSSYKDYMDTQIPALPKFPAKRFSLMVVQRLLATVAGYVDTPWYKKWYMKLK 278
         |:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    60 HPEATIREIASGYGEYMMTQVPAMTSFAERFSKMATKTLLVTVSDYVHLPAYKRWYRKFK 119

Qy   279 NFMVNRVFIPTKKFFNKEIREPSK-ALKEKVSTDTKDLFENKIGQGTVDFFNKEIRDPSK 337
         ||    |||  :||:|:||||  |||||||    |:||||||||||||| ||||
Db   120 EFIVN-FFTDPAKLIMKHVSQPVKTAYTKLVPEEHRQAIRDVVGQSTKHIAN-GVRDLAR 177

Qy   338 ALKEKVSNDAKDLFENKI-----GQGTVDFINNEIRDPSKALIRKVSTGAEDLFENKIG 391
         |:||  ||| |:|:||  ||||||||||:||  ||||||||
Db   178 MIKE-----PSQQIIREKLPHYLSKAKGAVEHVVDKVK--SKTLKKRAGESSEESYSD--- 228

Qy   392 QGTVDFINNEIRDPSKALIRKV-----YTEAD-----DLFENKIGQGTVDFINKEIRD 439
         ||||||||:||              ||  ||||
Db   229 -SEEEILKESQYNPAKSVAESADKDDYLYADWKDAALYKK---YNWVDGVGYEIKD 280
```

RESULT 29
```
ID   Q9GUD9      PRELIMINARY;      PRT;   301 AA.
AC   Q9GUD9;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   RAP-1 ALPHA-1 (FRAGMENT).
GN   RAP-1 ALPHA-1.
OS   Babesia bigemina.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX   NCBI_TaxID=5866;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S2P;
RX   MEDLINE=98135662; PubMed=9476795;
RA   Hotzel I., Suarez C.E., McElwain T.F., Palmer G.H.;
RT   "Genetic variation in the dimorphic regions of RAP-1 genes and rap-1
RT   loci of Babesia bigemina.";
RL   Mol. Biochem. Parasitol. 90:479-489(1997).
DR   EMBL; AF017287; AAG14905.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   301 AA;   33868 MW;   B162189C9668FCF6 CRC64;
```

```
Query Match             18.5%;     Score 437.5;   DB 5;    Length 301;
Best Local Similarity   37.8%;     Pred. No. 2.5e-21;
Matches 105; Conservative 47; Mismatches 97; Indels 29; Gaps 10;
```

```
Qy   159 FASRYLYMATLYYKTYTNVDEFGASFFNKLSFTTGLFGWGIKRALKQIIRSNLPLDIGTE 218
         |:|||:|||||||||||||||||||:||||::|:|||||||:|||:||||||||:|:||
Db     1 FASQYFYMTTLYYKTYLTVDFTAAKFFNKLAFTTRLFGFGIQKALKRLVRSNLPVDLGT- 59

Qy   219 HSVSRLQHITSSYKDYMDTQIPALPKFPAKRFSLMVVQRLLATVAGYVDTPWYKKWYMKLK 278
         |:||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    60 HPEATIREIASGYGEYMMTQVPAMTSFAERFSKMATKTLLVTVSDYVHLPAYKRWYRKFK 119

Qy   279 NFMVNRVFIPTKKFFNKEIREPSK-ALKEKVSTDTKDLFENKIGQGTVDFFNKEIRDPSK 337
```

```
Db  120  EFIVN-FFTDPAKLIMKHVSQPVKTAYTKLVPEEHRQAIRDVVGQSTKHIAN-GVRDLAR  177

Qy  338  ALKEKVSNDAKDLFENKI------GQGTVDFINNEIRD--PSKALIRKVSTGAEDLFENK  389

Db  178  MIKE----PSQOIIREKLPHYLSKAKGAVEHVVKKSVVPIK---QKGDQPSEAAVEET  230

Qy  390  IGQGTVDFINNEIRDPSKALIRKVYTE--------ADD  419

Db  231  VPSG--DSAETEEVPEEQYVDAVTEGVNSEKVDADD  266


RESULT 30
Q9GUD8
ID   Q9GUD8      PRELIMINARY;   PRT;   304 AA.
AC   Q9GUD8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   RAP-1 ALPHA-1 (FRAGMENT).
GN   RAP-1 ALPHA-1.
OS   Babesia bigemina.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX   NCBI_TaxID=5866;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98155662; PubMed=9476795;
RA   Hotzel I., Suarez C.E., McElwain T.F., Palmer G.H.;
RT   "Genetic variation in the dimorphic regions of RAP-1 genes and rap-1
RT   loci of Babesia bigemina.";
RL   Mol. Biochem. Parasitol. 90:479-489(1997).
DR   EMBL; AF017289; AAG14907.1; -.
FT   NON_TER      1
SQ   SEQUENCE   304 AA;  34195 MW;  04616ZDD5A48B8FE CRC64;

Query Match             18.5%;  Score 437.5;  DB 5;  Length 304;
Best Local Similarity   36.5%;   Pred. No. 2.6e-21;
Matches  115;  Conservative   51;  Mismatches  116;  Indels   33;  Gaps   13;

Qy  159  FASRYLYMATLYYKTYTNVDEEGCASFENKLSFTTGLFGWGIKRALKQIIRSNLPLDIGTE  218
Db    1  FASQYFYMTLLYYKTYLTLVDFTAAKFENKLAFTTRLFGFGIQKALKRLVRSNLPVDLGT-   59

Qy  219  HSVSRLQHITSSYKDYMDTQIPALPKFAKRFESLMVVQRLLATVAGYVDPTPWYKKWYMKLK  278
Db   60  HPEATIREIASGYGEYMMTQVPAMTSFAERFSKMATKTLLVTVSDYVHLPAYKRWYRKFK   119

Qy  279  NFMVNRVFIPTKKFFNKEIREPSK-ALKEKVSTDTKDLFENKIGQGTVDFFNKEIRDPSK   337
Db  120  EFIVN-FFTDPAKLIMKHVSQPVKTAYTKLVPEEHRQAIRDVVGQSTKHIAN-GVRDLAR   177

Qy  338  ALKEKVSNDAKDLFENKI------GQGTVDFINNEIRD--PSKALIRKVSTGAEDLFENK  389
Db  178  MIKE----PSQOIIREKLPHYLPKAKGAVEHVVKKSVVPIK---QKGDQPSEAGVEET   230

Qy  390  IGQGTVDFINNEIRDPSKALIRKVYT-------EADDLFENKIGQGTVDFINKEIR-D   439
Db  231  VPSG--DSAETEEVPEEQYVDAVTTQEVNSEKVDADDA-GNAETQOLPDAEN-EVRADD   286

Qy  440  PSKALIRKVSTEADN  454
Db  287  PKNEDSSSSSSSSDD  301


RESULT 31
Q9GNI5
ID   Q9GNI5      PRELIMINARY;   PRT;   263 AA.
AC   Q9GNI5;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   RAP1 BETA-2 (FRAGMENT).
GN   RAP-1 BETA-2.
OS   Babesia bigemina.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX   NCBI_TaxID=5866;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CGA;
RX   MEDLINE=98155662; PubMed=9476795;
RA   Hotzel I., Suarez C.E., McElwain T.F., Palmer G.H.;
RT   "Genetic variation in the dimorphic regions of RAP-1 genes and rap-1
RT   loci of Babesia bigemina.";
RL   Mol. Biochem. Parasitol. 90:479-489(1997).
DR   EMBL; AF017293; AAG14911.1; -.
DR   EMBL; AF017292; AAG14910.1; -.
FT   NON_TER      1
SQ   SEQUENCE   263 AA;  30250 MW;  15B60C13641ZAD6B CRC64;

Query Match             18.5%;  Score 437;  DB 5;  Length 263;
Best Local Similarity   38.7%;   Pred. No. 2.3e-21;
Matches   99;  Conservative   50;  Mismatches   85;  Indels   22;  Gaps    8;

Qy  159  FASRYLYMATLYYKTYTNVDEEGCASFENKLSFTTGLFGWGIKRALKQIIRSNLPLDIGTE  218
Db    1  FASQYFYMTLLYYKTYLTLVDFTAAKFENKLAFTTRLFGFGIQKALKRLVRSNLPVDLGT-   59

Qy  219  HSVSRLQHITSSYKDYMDTQIPALPKFAKRFESLMVVQRLLATVAGYVDPTPWYKKWYMKLK  278
Db   60  HPEATIREIASGYGEYMMTQVPAMTSFAERFSKMATKTLLVTVSDYVHLPAYKRWYRKFK   119

Qy  279  NFMVNRVFIPTKKFFNKEIREPSK-ALKEKVSTDTKDLFENKIGQGTVDFFNKEIRDPSK   337
Db  120  EFIVN-FFTDPAKLIMKHVSQPVKTAYTKLVPEEHRQAIRDVVGQSTKHIAN-GVRDLAR   177

Qy  338  ALKEKVSNDAKDLFENKI------GQGTVDFINNEIRDPSKALIRKVSTGAEDLFEN--  388
Db  178  MIKE----PSQOIIREKLPHYLSKAKGAVEHVDKVK--SKTLKKRAGESSBEESYSDSEE  231

Qy  389  ---KIGQGTVDFINNE  401
Db  232  EILKESQYNSDRENDE  247


RESULT 32
Q9GUD6
ID   Q9GUD6      PRELIMINARY;   PRT;   263 AA.
AC   Q9GUD6;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   RAP1 BETA-2 (FRAGMENT).
GN   RAP1 BETA-2.
OS   Babesia bigemina.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX   NCBI_TaxID=5866;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98155662; PubMed=9476795;
RA   Hotzel I., Suarez C.E., McElwain T.F., Palmer G.H.;
RT   "Genetic variation in the dimorphic regions of RAP-1 genes and rap-1
RT   loci of Babesia bigemina.";
RL   Mol. Biochem. Parasitol. 90:479-489(1997).
DR   EMBL; AF017294; AAG14912.1; -.
FT   NON_TER      1
SQ   SEQUENCE   263 AA;  30192 MW;  0725C313641462EA CRC64;

Query Match             18.5%;  Score 436;  DB 5;  Length 263;
Best Local Similarity   38.7%;   Pred. No. 2.7e-21;
Matches   99;  Conservative   50;  Mismatches   85;  Indels   22;  Gaps    8;

Qy  159  FASRYLYMATLYYKTYTNVDEEGCASFENKLSFTTGLFGWGIKRALKQIIRSNLPLDIGTE  218
Db    1  FASQYFYMTLLYYKTYLTLVDFTAAKFENKLAFTTRLFGFGIQKALKRLVRSNLPVDLGT-   59
```

```
Qy    219  HSVSRLQHITSSYKDYMDTQIPALPKFAKRFSLMVVQRLLATVAGYVDTPWYKKWYMKLK  278
                |.|:||.||||.||  |.|| ||.|| |.|||||.:.||||| :||||.|| ||:|||
Db     60  HPEATIREIASGYGEYMMTQVPAMTSFAERFSKMATKTLLVTVSDYVHLPAYKRWYRKFK  119

Qy    279  NFMVNRVFIPTKKFFNKEIREPSK-ALKEKVSTDTKDLFENKIGQGTVDFINNEIRDPSK  337
                |:|| ||||||.||||.|:.||  .|||:|.:.|  ||:||.|||||||||||.|| |
Db    120  EFIVN-FFTDPAKLIMKHVSQPVKTAYTKLVPEEHRQAIRDVVGQSTKHIAN--GVRDLAR  177

Qy    338  ALKEKVSNDAKDLFENKI------GGQGTVDFINNEIRDPSKALIRKVSTGAEDLFEN---  388
                ||:|.| :.||.|||  :||   |:|| |||||||||.|| ||.|:.||| |:.
Db    178  MIKE-----PSQQIIREKLPHYLSKAKGAVEHVVDKVK--SKTLKKRAGESSEESYSDSEE  231

Qy    389  ---KIGQGTVDFINNE  401
              |:|||.||||||
Db    232  EILKESQYNSDRENDE  247
```

RESULT 33

```
Q9GNG3

ID    Q9GNG3                PRELIMINARY;    PRT;    304 AA.
AC    Q9GNG3;
DT    01-MAR-2001 (TrEMBLrel. 16, Created)
DT    01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT    01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE    RAP-1 ALPHA-1 (FRAGMENT).
GN    RAP-1 BETA-3.
OS    Babesia bigemina.
OC    Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX    NCBI_TaxID=5866;
RN    [1]
RP    SEQUENCE FROM N.A.
RC    STRAIN=PUERTO RICO, CGP, S1A, AND TEXCOCO;
RX    MEDLINE=98135662; PubMed=9476795;
RA    Hotzel I., Suarez C.E., McElwain T.F., Palmer G.H.;
RT    "Genetic variation in the dimorphic regions of RAP-1 genes and rap-1
RT    loci of Babesia bigemina.";
RL    Mol. Biochem. Parasitol. 90:479-489(1997).
DR    EMBL; AF017290; AAG14908.1; -.
DR    EMBL; AF017285; AAG14903.1; -.
DR    EMBL; AF017286; AAG14904.1; -.
DR    EMBL; AF017288; AAG14906.1; -.
FT    NON_TER        1
SQ    SEQUENCE   304 AA;  39287ZB344D88399 CRC64;
```

```
Qy    159  FASRYLYMATLIYKTYTNVDEFGASFENKLSFTTGLFGWGIKRALKQIIRSNLPLDIGTE  218
                |:|:|.| || |||.:|:|||||.:|||.||:.||.||||:::|||:::: :|:|||.
Db      1  FASQYFYMTTLIYKTYLTVDFTAAKFFNKLAFTTRLFGFGIQKALKRLVRSNLPVDLGT-   59

Best Local Similarity   18.5%;
Matches  114;  Conservative  52;  Mismatches  116;  Indels  33;  Gaps  13;
Query Match   36.2%;  Score 435.5;  DB 5;  Length 304;
                 Pred. No. 3.5e-21;
```

```
Qy    219  HSVSRLQHITSSYKDYMDTQIPALPKFAKRFSLMVVQRLLATVAGYVDTPWYKKWYMKLK  278
                |.|:||.||||.||  |.|| ||.|| |.|||||.:.||||| :||||.|| ||:|||
Db     60  HPEATIREIASGYGEYMMTQVPAMTSFAERFSKMATKTLLVTVSDYVHLPAYKRWYRKFK  119

Qy    279  NFMVNRVFIPTKKFFNKEIREPSK-ALKEKVSTDTKDLFENKIGQGTVDFINNEIRDPSK  337
                |:|| ||||||.||||.|:.||  .|||:|.:.|  ||:||.|||||||||||.|| |
Db    120  EFIVN-FFTDPAKLIMKHVSQPVKTAYTKLVPEEHRQAIRDVVGQSTKHIAN--GVRDLAR  177

Qy    338  ALKEKVSNDAKDLFENKI------GGQGTVDFINNEIRDPSKALIRKVSTGAEDLFENK   389
                ||:|.| :.||.|||  :||  |:|| ||||||||||.|| ||.|:.||| |:.
Db    178  MIKE-----PSQQIIREKLPHYLSKAKGAVEHVVDKVK--SKTLKKRAGESSEESYSD-- 228
```

RESULT 34

```
Q9GUD2

ID    Q9GUD2                PRELIMINARY;    PRT;    282 AA.
AC    Q9GUD2;
DT    01-MAR-2001 (TrEMBLrel. 16, Created)
DT    01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT    01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE    RAP1 BETA-3 (FRAGMENT).
GN    RAP-1 BETA-3.
OS    Babesia bigemina.
OC    Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX    NCBI_TaxID=5866;
RN    [1]
RP    SEQUENCE FROM N.A.
RC    STRAIN=TEXCOCO;
RX    MEDLINE=98135662; PubMed=9476795;
RA    Hotzel I., Suarez C.E., McElwain T.F., Palmer G.H.;
RT    "Genetic variation in the dimorphic regions of RAP-1 genes and rap-1
RT    loci of Babesia bigemina.";
RL    Mol. Biochem. Parasitol. 90:479-489(1997).
DR    EMBL; AF017298; AAG14916.1; -.
FT    NON_TER        1
SQ    SEQUENCE   282 AA;  9E23CCD5C3387BCB CRC64;
```

```
Qy    159  FASRYLYMATLIYKTYTNVDEFGASFENKLSFTTGLFGWGIKRALKQIIRSNLPLDIGTE  218
                |:|:|.| || |||.:|:|||||.:|||.||:.||.||||:::|||:::: :|:|||.
Db      1  FASQYFYMTTLIYKTYLTVDFTAAKFFNKLAFTTRLFGFGIQKALKRLVRSNLPVDLGT-   59

Qy    219  HSVSRLQHITSSYKDYMDTQIPALPKFAKRFSLMVVQRLLATVAGYVDTPWYKKWYMKLK  278
                |.|:||.||||.||  |.|| ||.|| |.|||||.:.||||| :||||.|| ||:|||
Db     60  HPEATIREIASGYGEYMMTQVPAMTSFAERFSKMATKTLLVTVSDYVHLPAYKRWYRKFK  119

Qy    279  NFMVNRVFIPTKKFFNKEIREPSK-ALKEKVSTDTKDLFENKIGQGTVDFINNEIRDPSK  337
                |:|| ||||||.||||.|:.||  .|||:|.:.|  ||:||.|||||||||||.|| |
Db    120  EFIVN-FFTDPAKLIMKHVSQPVKTAYTKLVPEEHRQAIRGVVGQSTKHIAN--GVRDLAR  177

Qy    338  ALKEKVSNDAKDLFENKI------GGQGTVDFINNEIRDPSKALIRKVSTGAEDLFENKIG  391
                ||:|.| :.||.|||  :||  |:|| ||||||||||.|| ||.|:.||| |:.
Db    178  MIKE-----PSQQIIREKLPHYLSKAKGAVEHVVDKVK--SKTLKKRAGESSEESYSD--  228

Qy    392  QGTVDFINNEIRDPSKALIRKV----YTEAD----DLFENKIGQGTVDFINKEIRD  439
                |||||||||.|| ||.|:.||    |:||    :|||||.|||::||||||:||.
Db    229  -SEEEILKESQYNPAKSVAESADKDDLYADWKDAALYKK---YNWVDGVGYEIKD  280

Best Local Similarity   18.4%;
Matches  103;  Conservative  60;  Mismatches  102;  Indels  31;  Gaps  11;
Query Match   34.8%;  Score 433.5;  DB 5;  Length 282;
                 Pred. No. 4.3e-21;
```

RESULT 35

```
Q9GUE0

ID    Q9GUE0                PRELIMINARY;    PRT;    304 AA.
AC    Q9GUE0;
DT    01-MAR-2001 (TrEMBLrel. 16, Created)
DT    01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT    01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE    RAP-1 ALPHA-1 (FRAGMENT).
GN    RAP-1 ALPHA-1.
OS    Babesia bigemina.
OC    Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX    NCBI_TaxID=5866;
RN    [1]
RP    SEQUENCE FROM N.A.
RC    STRAIN=CGA;
RX    MEDLINE=98135662; PubMed=9476795;
RA    Hotzel I., Suarez C.E., McElwain T.F., Palmer G.H.;
RT    "Genetic variation in the dimorphic regions of RAP-1 genes and rap-1
RT    loci of Babesia bigemina.";
RL    Mol. Biochem. Parasitol. 90:479-489(1997).
DR    EMBL; AF017284; AAG14902.1; -.
FT    NON_TER        1
SQ    SEQUENCE   304 AA;  34227 MW;  B577BA50D96319FD CRC64;
```

```
Query Match
Best Local Similarity   35.9%;            Score 432.5; DB 5; Length 304;
Matches 113; Conservative 53; Mismatches 116;   Pred. No. 5.5e-21; Indels 33; Gaps 13;

Qy  159 FASRYLYMATLLYKYKTYTNVDEFGASFFNKLSFTTGLLFGWGIKRALKQIIRSNLPLDIGTE 218
         |||:|| ||||||||| |||:||
Db    1 FASQYFMTLLYYKLYTLTVDFTAAKFFNKLAFTTRLFGFGIQKALRLVRSNLPVDLGT-    59

Qy  219 HSVSRLQHITSSYKDYMDTQIPALPKFAKRFSLMVVQRLLATVAGYDTPWYKKWYMKLK    278
         ||:|| :|| ::|| |::|||:||
Db   60 HPEATIREIASGYEVMMTQVPAMTSFAERFSKMATKTLLVTSDYVHLPAYKRWYRKFK     119

Qy  279 NFMVNRVFIPTKKFFNKEIREPSK-ALKEKVSTDTKDLFENKIGQGTVDFFNKEIRDPSK    337
         ||::|| || |:|| :|| ||
Db  120 EFIVN-FFTDPARLIMKHVSQPVKTAYTKLVPEEHRQAIRDVVGQSTKHIAN-GVRDLAR   177

Qy  338 ALKEKVSNDAKDLFENKI------GQGTVDFINNEIRD--PSKALIRKVSTGAEDLFENK   389
         :|| ::|| :|::||
Db  178 MIKE-----PSQQIIREKLPHYLSKAKGAVEHVVKVKSVVPIK---QKGDQPSEAAVEET  230

Qy  390 IGQGTVDFINNEIRDPSKALIRKVYT-------------EADDLFENKIGQGTVDFINKEIR--D 439
         |::|| :|::||::| ::|| : ||
Db  231 VPSG--DSAETEFEVPEEQYVDAVTTQQVNSEKVDADDA-GNAETQQLPDAEN-EVRADD  286

Qy  440 PSKALIRKVSTEADN 454
         ::| :
Db  287 PKNEDSSSSSSSDD  301
```

RESULT 36

```
ID   Q9GUD7      PRELIMINARY;     PRT;    304 AA.
AC   Q9GUD7;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE   RAP-1 ALPHA-1 (FRAGMENT).
GN   RAP-1 ALPHA-1.
OS   Babesia bigemina.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX   NCBI_TaxID=5866;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98135662; PubMed=9476795;
RA   Hotzel I., Suarez C.E., McElwain T.F., Palmer G.H.;
RT   "Genetic variation in the dimorphic regions of RAP-1 genes and rap-1
RT   loci of Babesia bigemina.";
RL   Mol. Biochem. Parasitol. 90:479-489(1997).
DR   EMBL; AF017291; AAG14909.1; -.
SQ   SEQUENCE   304 AA;  34193 MW;  60F01A976FB0FA22 CRC64;
```

```
Query Match
Best Local Similarity   36.3%;            Score 431.5; DB 5; Length 304;
Matches 113; Conservative 51; Mismatches 122;   Pred. No. 6.4e-21; Indels 25; Gaps 12;

Qy  159 FASRYLYMATLLYKYKTYTNVDEFGASFFNKLSFTTGLLFGWGIKRALKQIIRSNLPLDIGTE 218
         |||:|| ||||||||| |||:||
Db    1 FASQYFMTLLYYKLYTLTVDFTAAKFFNKLAFTTRLFGFGIQKALRLVRSNLPVDLGT-    59

Qy  219 HSVSRLQHITSSYKDYMDTQIPALPKFAKRFSLMVVQRLLATVAGYDTPWYKKWYMKLK    278
         ||:|| :|| ::|| |::|||:||
Db   60 HPEATIREIASGYEVMMTQVPAMTSFAERFSKMATKTLLVTSDYVHLPAYKRWYRKFK     119

Qy  279 NFMVNRVFIPTKKFFNKEIREPSK-ALKEKVSTDTKDLFENKIGQGTVDFFNKEIRDPSK    337
         ||::|| || |:|| :|| ||
Db  120 EFIVN-FFTDPAKLIMKHVSQPVKTAYTKLVPEEHRQAIRDVVGQSTKHIAN-GVRDLAR   177

Qy  338 ALKEKVSNDAKDLFENKI--GQGTVDFINNEIRD--PSKALIRKVSTGAEDLFENKIGQG  393
         :|| ::|| :|::||
Db  178 MIKEPSQQIIRERLPHYLSKARGAVEHVVKVKSVVPIK--QKGDQPSEAAVEETVPSG    234
```

```
Qy  394 TVDFINNEIRDPSKALIRKVYT--------EADDLFENKIGQGTVDFINKEIR--DPSKA  443
         |::|| :|::||::| ||
Db  235 --DSAETEFEVPEEQYVDAVTTQQVNSEKVDADDA-GNAETQQLPDAEN-EVRADDPQNE  290

Qy  444 LIRKVSTEADN 454
         :|:
Db  291 DSSSSSSSSDD 301
```

RESULT 37

```
ID   Q27305      PRELIMINARY;     PRT;    133 AA.
AC   Q27305;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   RHOPTRY PROTEIN (FRAGMENT).
OS   Babesia ovis.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX   NCBI_TaxID=5869;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Dalrymple B.P., Casu R.E., Peters J.M., Dimmock C., Gale K.R.,
RA   Bose R., Wright I.G.;
RL   Submitted (SEP-1992) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Dalrymple B.P., Casu R.E., Peters J.M., Dimmock C., Gale K.R.,
RA   Bose R., Wright I.G.;
RL   Submitted (AUG-1992) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; M91176; AAA27813.1; -.
DR   EMBL; M91172; AAA27801.1; -.
DR   InterPro; IPR004318; -.
DR   Pfam; PF03085; RAP-1; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   133 AA;  15661 MW;  7F587B31DAFAD1D4 CRC64;
```

```
Query Match
Best Local Similarity   54.9%;            Score 403.5; DB 5; Length 133;
Matches 73; Conservative 30; Mismatches 29;   Pred. No. 1.5e-19; Indels 1; Gaps 1;

Qy  164 LYMATLLYKYKTYTNVDEFGASFFNKLSFTTGLLFGWGIKRALKQIIRSNLPLDIGTEHSVSR 223
         ||||| :|| |||||: ||||| |:||||||:||
Db    2 LYMATTYYKRYLIVNNSDAKFFNRIAFAFATKIFGFGIKKALKDIVRSNVPEYMG-EHSIER   60

Qy  224 LQHITSSYKDYMDTQIPALPKFAKRFSLMVVQRLLATVAGYDTPWYKKWYMKLKNFMVN    283
         : |||||:|| ||||:||| |:|::|||:||
Db   61 ISHLAHGYKDYMLTQVPTLSKFAERYSDMVMKVLLSSLAGYVKAPWYKRWFNKVKDFYVN   120

Qy  284 RVFIPTKKFFNKE 296
         :|: |||
Db  121 KIGKPTKEHFHKK 133
```

RESULT 38

```
ID   Q17258      PRELIMINARY;     PRT;    192 AA.
AC   Q17258;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   RHOPTRY PROTEIN (FRAGMENT).
OS   Babesia ovis.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX   NCBI_TaxID=5869;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93165069; PubMed=8433711;
RA   Dalrymple B.P., Casu R.E., Peters J.M., Dimmock C., Gale K.R., Bose R.,
RA   Wright I.G.;
RT   "Characterisation of a family of multi-copy genes encoding rhoptry
```

RT   protein homologues in Babesia bovis, Babesia ovis and Babesia canis.";
RL   Mol. Biochem. Parasitol. 57:181-192(1993).
DR   EMBL; M91173; AAA27812.1; -.
DR   InterPro; IPR004318; RAP-1.
DR   Pfam; PF03085; RAP-1; 1.
FT   NON_TER   192
FT   NON_TER   192
SQ   SEQUENCE   192 AA; MW; 78539B83686CBC12 CRC64;

Query Match   15.5%; Score 365; DB 5; Length 192;
Best Local Similarity   43.3%; Pred. No. 8.4e-17;
Matches   68; Conservative   30; Mismatches   59; Indels   0; Gaps   0;

Qy   1 MAPSDSVGDVTKTLLAASESVDSAANAYMINSDMSDYLSAVSDNEAERICSQVPKGSNCS 60
Db   31 LAPAEVGNVAATLSTADEIISSHDYDKELINDMRDQMREMGENEVDTVCTKAPEDSNCR 90

Qy   61 ASVSAYMSRCAKQDCLTLQSLKYPLEAKYQPLTLEDPYQLEAAFILFKESDANPANSTEK 120
Db   91 QMVALYADRCEMYGCLQIDNVNYPVDEEYQPLSLENPYQLDAAFTLFKNSASNPAKNGLK 150

Qy   121 RFWMRFRRGKNHSYFHDLVFNLLEKNVTRDADATDIE 157
Db   151 GQWMRFRNCKKHGDYHRFLIGLLAKGVTRKDGATDLE 187

RESULT 39
ID   O96431
AC   O96431;   PRELIMINARY;   PRT;   69 AA.
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE   PUTATIVE MEROZOITE SURFACE PROTEIN (FRAGMENT).
OS   Babesia caballi.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX   NCBI_TaxID=5871;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hentrich B., Boese R.;
RT   "Expression and preliminary characterization of cDNA sequences of
RT   Babesia caballi.";
RL   Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF048748; AAD02477.1; -.
KW   Merozoite.
FT   NON_TER   1
SQ   SEQUENCE   69 AA; 7792 MW; D4D91BB408F55BDE CRC64;

Query Match   100.0%; Score 346; DB 5; Length 69;
Best Local Similarity   100.0%; Pred. No. 4e-16;
Matches   69; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   390 IGQGTVDFINNEIRDPSKALIRKVYTEADLFENKIGQGTVDFINKEIRDPSKALIRKVS 449
Db   1 IGQGTVDFINNEIRDPSKALIRKVYTEADLFENKIGQGTVDFINKEIRDPSKALIRKVS 60

Qy   450 TEADNLLEK 458
Db   61 TEADNLLEK 69

RESULT 40
ID   P90650
AC   P90650;   PRELIMINARY;   PRT;   62 AA.
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   BCAB60 (FRAGMENT).
OS   Babesia caballi.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX   NCBI_TaxID=5871;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=USDA;
RX   MEDLINE=97043665; PubMed=8887337;
RA   Dalrymple B.P., Peters J.M., Bose R., Wright I.G.;
RT   "A polymerase chain reaction method for the identification of genes
RT   encoding members of the Bv60/p58 family of rhoptry protein homologues
RT   in the genus Babesia.";
RL   Exp. Parasitol. 84:96-100(1996).
DR   EMBL; U46551; AAB53239.1; -.
FT   NON_TER   1
FT   NON_TER   62
SQ   SEQUENCE   62 AA; 7507 MW; EE56982C608313E4 CRC64;

Query Match   14.0%; Score 331; DB 5; Length 62;
Best Local Similarity   100.0%; Pred. No. 3.4e-15;
Matches   62; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   104 FILFKESDANPANSTEKRFWMRFRRGKNHSYFHDLVFNLLEKNVTRDADATDIENFASRY 163
Db   1 FILFKESDANPANSTEKRFWMRFRRGKNHSYFHDLVFNLLEKNVTRDADATDIENFASRY 60

Qy   164 LY 165
Db   61 LY 62

Search completed: October 19, 2002, 07:51:12
Job time : 70 secs